

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 9, 2006, 10:49:49 ; Search time 23 Seconds
(without alignments)
1543.652 Million cell updates/sec

Title: US-10-633-631-2

Perfect score: 369

Sequence: 1 MYAMKYNKQOCIERDEVN.....EAERSALPMCGPICPSAGSG 369

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

PIR 80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	3.5	338	2 T41021	ser-thr protein ki
2	12	3.3	379	2 T23688	hypothetical prote
3	9	2.4	151	2 PC4223	rho kinase - pig {
4	9	2.4	251	2 G75345	serine/threonine-p
5	9	2.4	415	2 G01876	casein kinase I de
6	9	2.4	416	2 I61744	casein kinase I-ep
7	9	2.4	428	2 A46002	casein kinase I (E
8	9	2.4	546	2 AI2045	serine/threonine k
9	9	2.4	1173	2 T25539	hypothetical prote
10	9	2.4	1354	2 S74244	serine/threonine-s
11	9	2.4	1354	2 S69211	serine/threonine-s
12	9	2.4	1388	2 S70633	serine/threonine-s
13	9	2.4	1388	2 S74245	serine/threonine-s
14	8	2.2	258	2 H88130	protein Fl0G7.3 [I
15	8	2.2	282	2 D84375	ATP phosphoribosyl
16	8	2.2	351	2 T06749	hypothetical prote
17	8	2.2	363	2 T22107	hypothetical prote
18	8	2.2	393	2 A45176	protein kinase Dco
19	8	2.2	412	2 I78395	myotonic dystrophy
20	8	2.2	441	2 I78393	myotonic dystrophy
21	8	2.2	474	2 I78396	myotonic dystrophy
22	8	2.2	480	2 T47255	serine/threonine k
23	8	2.2	516	2 I78394	myotonic dystrophy
24	8	2.2	557	2 S71829	serine/threonine-s
25	8	2.2	582	2 A96713	hypothetical prote
26	8	2.2	598	2 T47254	serine/threonine k
27	8	2.2	605	2 S18648	protein kinase wis
28	8	2.2	614	2 F97381	hypothetical prote
29	8	2.2	614	2 AE2599	hypothetical prote

30 8 2.2 620 2 S22711 probable protein k
31 8 2.2 622 2 T10009 probable serine/th
32 8 2.2 622 2 H86910 probable serine/th
33 8 2.2 624 2 B49364 protein kinase (EC
34 8 2.2 626 1 D70699 probable pknB prot
35 8 2.2 665 2 S70706 probable protein k
36 8 2.2 668 2 S58909 polymyxin B resist
37 8 2.2 1548 2 T25808 hypothetical prote
38 7 1.9 126 2 S52255 copper resistance
39 7 1.9 128 1 NROW2 pancreatic ribonuc
40 7 1.9 149 2 S39910 S-receptor kinase
41 7 1.9 150 2 S31411 S-receptor kinase
42 7 1.9 151 2 F98296 hypothetical prote
43 7 1.9 151 2 AB2987 hypothetical prote
44 7 1.9 154 2 T50898 hypothetical prote
45 7 1.9 162 2 S71633 MAP kinase kinase

ALIGNMENTS

RESULT 1

T41021
ser-thr protein kinase - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T41021
R:Murphy, L.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, June 1998
A:Reference number: Z21965
A:Accession: T41021
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-338 <MUR>
A:Cross-references: UNIPROT:O74426; UNIPARC:UPI0000069FF8; EMBL:AL023860; PIDN:CAA19590.1
A:Experimental source: strain 972h; cosmid c162
C:Genetics:
A:Gene: SPDB:SPCC162.10
A:Map position: 3
C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 3.5%; Score 13; DB 2; Length 338;
Best Local Similarity 100.0%; Pred. No. 7.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 HRDVKPDNILLDE 109
DB 149 HRDVKPDNILLDE 161

RESULT 2

T23688
hypothetical protein M03C11.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23688
R:McMurray, A.
submitted to the EMBL Data Library, April 1995
A:Reference number: Z19783
A:Accession: T23688
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-379 <WIL>
A:Cross-references: UNIPROT:Q21483; UNIPARC:UPI000007B6C1; EMBL:Z49128; PIDN:CAA88953.1.1
A:Experimental source: clone M03C11
C:Genetics:
A:Gene: CRSP:M03C11.1
A:Map position: 3
A:Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3
C:Superfamily: Kinase-related transforming protein; protein kinase homology

Query Match 3.3%; Score 12; DB 2; Length 379;
Best Local Similarity 100.0%; Pred. No. 0.00088;

```
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 DILLGGDLRYHL 65
Db 106 DLLLGGLDLYHL 117

RESULT 3
PC4223
rho kinase - pig (fragment)
A:Species: Sus scrofa domestica (domestic pig)
C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 05-Oct-2004
C:Accession: PC4223
R:Nishimura, J.; Sakihara, C.; Zhou, Y.; Kanaide, H.
Biochem. Biophys. Res. Commun. 227, 750-754, 1996
A:Title: Expression of rho A and rho kinase mRNAs in porcine vascular smooth muscle.
A:Reference number: PC4222; MUID:97040692; PMID:8886005
A:Accession: PC4223
A:Molecule type: mRNA
A:Residues: 1-151 <NIS>
A:Cross-references: UNIPROT:P79276; UNIPARC:UPI000017A471; DDBJ:D89493; NID:g1695732; PID:g1695732
C:Comment: This enzyme mediates the inhibitor of myosin light chain.
F:1-151/Domain: protein kinase homology (fragment) <KIN>

Query Match 2.4%; Score 9; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 IHRDVKPDN 104
Db 21 IHRDVKPDN 29

RESULT 4
G75345
serine/threonine-protein kinase-related protein - Deinococcus radiodurans (strain R1)
A:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: G75345
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: G75345
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-251 <WHI>
A:Cross-references: UNIPROT:Q9RTB4; UNIPARC:UPI00000D3EB4; GB:AE002025; GB:AE000513; NID:AE000513
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1851
A:Map position: 1

Query Match 2.4%; Score 9; DB 2; Length 251;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 HRDVKPDNI 105
Db 128 HRDVKPDNI 136

RESULT 5
G01876
casein kinase I delta - human
A:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C:Accession: G01876
R:Kusuda, J.
submitted to the EMBL Data Library, June 1995
A:Reference number: G08678
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A:Accession: G01876
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-415 <KUS>
A:Cross-references: UNIPROT:P48730; UNIPARC:UPI0000153EE7; EMBL:U29171; NID:g881618; PID:g881618
C:Superfamily: kinase-related transforming protein; protein kinase homology
F:7-279/Domain: protein kinase homology <KIN>

Query Match 2.4%; Score 9; DB 2; Length 415;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 IHRDVKPDN 104
Db 125 IHRDVKPDN 133

RESULT 6
I61744
casein kinase I-epsilon - human
A:Species: Homo sapiens (man)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C:Accession: I61744
R:Fish, K.J.; Cegielska, A.; Getman, M.E.; Landes, G.M.; Virshup, D.M.
J. Biol. Chem. 270, 14875-14883, 1995
A:Title: Isolation and characterization of human casein kinase I epsilon (CKI), a novel
A:Reference number: A57011; MUID:95318039; PMID:7797465
A:Accession: I61744
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-416 <RES>
A:Cross-references: UNIPROT:P49674; UNIPARC:UPI000012DC67; GB:L37043; NID:g852056; PID:g852056
C:Genetics:
A:Gene: GDB:CSNK1E; HCKIE
A:Cross-references: GDB:604574; OMIM:600863
A:Map position: 22q12-22q13
C:Superfamily: Kinase-related transforming protein; protein kinase homology
F:7-279/Domain: protein kinase homology <KIN>

Query Match 2.4%; Score 9; DB 2; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 IHRDVKPDN 104
Db 125 IHRDVKPDN 133

RESULT 7
A46002
casein kinase I (EC 2.7.1.-) delta, 49K isoform - rat
A:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A46002
R:Graves, P.R.; Haas, D.W.; Hagedorn, C.H.; DePaoli-Roach, A.A.; Roach, P.J.
J. Biol. Chem. 268, 6394-6401, 1993
A:Title: Molecular cloning, expression, and characterization of a 49-kilodalton casein ki
A:Reference number: A46002; MUID:93203231; PMID:8454611
A:Accession: A46002
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-428 <GRA>
A:Cross-references: UNIPROT:Q06486; UNIPARC:UPI000012DC66; GB:L07578; NID:g294524; PID:g294524
A:Experimental source: testis
A:Note: sequence extracted from NCBI backbone (NCBIN:127927, NCBI:P127928)
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: phosphotransferase; serine/threonine-specific protein kinase
F:7-279/Domain: protein kinase homology <KIN>

Query Match 2.4%; Score 9; DB 2; Length 428;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 96 IHRDVKPDN 104
Db 125 IHRDVKPDN 133

RESULT 8
AI2045
serine/threonine kinase [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AI2045
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AI2045
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-546 <KUR>
A;Cross-references: UNIPROT:Q8YVQ5; UNIPARC:UPI00000CE25F; GB:BA000019; PIDN:BAB73618.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all1919

Query Match 2.4%; Score 9; DB 2; Length 546;
Best Local Similarity 100.0%; Pred. No. 1.4; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 97 HRDVKPDN 105
Db 137 HRDVKPDN 145

RESULT 9
T25539
hypothetical protein C10H11.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25539
R;Pante, M.; Wamaley, P.
Submitted to the EMBL Data Library, February 1997
A;Description: The sequence of C. elegans cosmid C10H11.
A;Reference number: Z20047
A;Accession: T25539
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1173 <DAN>
A;Cross-references: UNIPROT:P92199; UNIPARC:UPI00000804C8; EMBL:U88311; PIDN:AAB42348.1;
A;Experimental source: strain Bristol N2; clone C10H11
C;Genetics:
A;Gene: CESP:C10H11.9
A;Map position: 1
A;Introns: 23/3; 51/1; 104/3; 343/1; 478/2; 868/3; 891/3; 970/3; 1027/3; 1114/1
C;Superfamily: hypothetical protein C10H11.9; protein kinase homology

Query Match 2.4%; Score 9; DB 2; Length 1173;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 96 IHRDVKPDN 104
Db 187 IHRDVKPDN 195

RESULT 10
S74244
serine/threonine-specific protein kinase (EC 2.7.1.-) isoform I, Rho-associated - mouse
C;Species: Mus musculus (house mouse)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 05-Oct-2004
C;Accession: S74244
R;Nakagawa, O.; Fujisawa, K.; Ishizaki, T.; Saito, Y.; Nakao, K.; Narumiya, S.

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FBBS Lett. 392, 189-193, 1996
A;Title: ROCK-I and ROCK-II, two isoforms of Rho-associated coiled-coil forming protein
A;Reference number: S74244; MUID:96368048; PMID:8772201
A;Accession: S74244
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1354 <NAK>
A;Cross-references: UNIPROT:P70335; UNIPARC:UPI0000020720; EMBL:U58512; NID:g1514695; PFI
C;Keywords: coiled coil; phosphotransferase; serine/threonine-specific protein kinase
F;74-338/Domain: protein kinase homology <KIN>
F;1229-1283/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match 2.4%; Score 9; DB 2; Length 1354;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 96 IHRDVKPDN 104
Db 195 IHRDVKPDN 203

RESULT 11
S69211
serine/threonine-specific protein kinase (EC 2.7.1.-), Rho-associated - human
C;Species: Homo sapiens (man)
C;Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 31-Dec-2004
C;Accession: S69211; S71910
R;Ishizaki, T.; Maekawa, M.; Fujisawa, K.; Okawa, K.; Iwamatsu, A.; Fujita, A.; Watanabe
EMBO J. 15, 1885-1893, 1996
A;Title: The small GTP-binding protein Rho binds to and activates a 160 kDa Ser/Thr prot
A;Reference number: S69211; MUID:96203110; PMID:8617235
A;Accession: S69211
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1354 <ISH1>
A;Cross-references: UNIPROT:Q13464; UNIPARC:UPI000006F0A4; EMBL:U43195; NID:g1276900; PFI
A;Accession: S71910
A;Molecule type: protein
A;Residues: 187-195;281-288;465-473;573-587;818-828;885-893;934-945 <ISH2>
A;Cross-references: UNIPARC:UPI000017A400; UNIPARC:UPI000017A401; UNIPARC:UPI000017A402;
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;74-338/Domain: protein kinase homology <KIN>
F;82-90/Region: protein kinase ATP-binding motif
F;1229-1283/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match 2.4%; Score 9; DB 2; Length 1354;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 96 IHRDVKPDN 104
Db 195 IHRDVKPDN 203

RESULT 12
S70633
serine/threonine-specific protein kinase (EC 2.7.1.-), Rho-associated - bovine
N;Alternate names: Rho-associated protein kinase
C;Species: Bos primigenius taurus (cattle)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 31-Dec-2004
C;Accession: S70633; S77694
R;Matsui, T.; Amano, M.; Yamamoto, T.; Chihara, K.; Nakafuku, M.; Ito, M.; Nakano, T.; O
EMBO J. 15, 2208-2216, 1996
A;Title: Rho-associated kinase, a novel serine/threonine kinase, as a putative target fo
A;Reference number: S70633; MUID:96208507; PMID:8641286
A;Accession: S70633
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1388 <MAT1>
A;Cross-references: UNIPROT:Q28021; UNIPARC:UPI0000086C59; EMBL:U36909; NID:g1326077; PFI
A;Accession: S77694
A;Molecule type: protein
A;Residues: 1-18;30-34;36-44;58-64;133-140;248-252;291-295;327-347;350-360;366-3

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-1070 <MAT2>
A:Cross-references: UNIPARC:UPI000017A40B; UNIPARC:UPI000017A40C; UNIPARC:UPI000017A40D;
412; UNIPARC:UPI000017A413; UNIPARC:UPI000017A414; UNIPARC:UPI000017A415; UNIPARC:UPI000
1000017A41B; UNIPARC:UPI000017A41C; UNIPARC:UPI000017A41D; UNIPARC:UPI000017A41E; UNIPAR
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:90-354/Domain: protein kinase homology <KIN>
F:98-106/Region: protein kinase ATP-binding motif
F:1261-1315/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match      2.4%; Score 9; DB 2; Length 1388;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 IHRDVKPDN 104
    |||||
Db 211 IHRDVKPDN 219

RESULT 13
S74245
serine/threonine-specific protein kinase (EC 2.7.1.1-) isoform II, Rho-associated - mouse
C:Species: Mus musculus (house mouse)
C>Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 31-Dec-2004
C:Accession: S74245
R:Nakagawa, O.; Fujisawa, K.; Ishizaki, T.; Saito, Y.; Nakao, K.; Narumiya, S.
FEBS Lett. 392, 189-193, 1996
A>Title: ROCK-I and ROCK-II, two isoforms of Rho-associated coiled-coil forming protein
A:Reference number: S74244; MUID:96368048; PMID:8772201
A:Accession: S74245
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1388 <NAK>
A:Cross-references: UNIPROT:P70336; UNIPARC:UPI0000027021; EMBL:U58513; NID:gl514697; PI
F:90-354/Domain: protein kinase homology <KIN>
F:1261-1315/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match      2.4%; Score 9; DB 2; Length 1388;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 IHRDVKPDN 104
    |||||
Db 211 IHRDVKPDN 219

RESULT 14
H88130
protein F10G7.3 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H88130
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A>Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A:Reference number: A75000; MUID:99069613; PMID:9851916
A>Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_ele
A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: H88130
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <STO>
A:Cross-references: UNIPROT:Q19326; UNIPARC:UPI0000081869; GB:chr_II; PIDN:AA81128.1; PI
C:Genetics:
A:Gene: F10G7.3
A:Map position: 2

Query Match      2.2%; Score 8; DB 2; Length 258;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 344 ARPVEDEA 351
    |||||

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Db 144 ARPVEDEA 151

RESULT 15

D84375

ATP phosphoribosyltransferase [imported] - Halobacterium sp. NRC-1

C:Species: Halobacterium sp. NRC-1

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: D84375

R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leitchauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li

A>Title: Genome sequence of Halobacterium species NRC-1.

A:Reference number: A84160; MUID:20504483; PMID:11016950

A:Accession: D84375

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-282 <STO>

A:Cross-references: UNIPROT:Q9HNS3; UNIPARC:UPI000012C744; GB:AE004437; NID:gl0581661; P

C:Genetics:

A:Gene: hisG

C:Superfamily: ATP phosphoribosyltransferase; ATP phosphoribosyltransferase homology

Query Match 2.2%; Score 8; DB 2; Length 282;

Best Local Similarity 100.0%; Pred. No. 7.9;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 254 VPNGKGRLLH 261

|||

Db 5 VPNGKGRLLH 12

Search completed: May 9, 2006, 10:50:33

Job time : 24 secs

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OM protein - protein search, using sw model

Run on: May 9, 2006, 10:49:27 ; Search time 230 Seconds
(without alignments)
1131.913 Million cell updates/sec

Title: US-10-633-631-2
Perfect score: 369
Sequence: 1 MYAMKYNKQOCIERDEVRN.....EAERSALPMGCPICPSAGSG 369

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 1
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt_05.80:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	369	100.0	369	2	Q5TQ05_HUMAN
2	369	100.0	486	2	Q86UX6_HUMAN
3	300	81.3	381	2	Q5TQ04_HUMAN
4	268	72.6	369	2	Q86UE1_HUMAN
5	113	30.6	488	2	Q8QZV4_MOUSE
6	113	30.6	488	2	Q9JTG4_MOUSE
7	79	21.4	368	2	Q9BGT4_MACFA
8	67	18.2	441	2	Q4RN62_TETNG
9	35	9.5	166	2	Q8WU08_HUMAN
10	35	9.5	364	2	Q6UXH3_HUMAN
11	35	9.5	368	2	Q7TPQ4_MOUSE
12	35	9.5	396	2	Q5RAZ7_PONPY
13	35	9.5	396	2	Q6GQ72_XENLA
14	35	9.5	398	2	Q8BGW6_MOUSE
15	35	9.5	414	2	Q8IY14_HUMAN
16	35	9.5	414	2	Q9NT57_HUMAN
17	35	9.5	414	2	Q7TMD3_MOUSE
18	35	9.5	414	2	Q8C4E0_MOUSE
19	35	9.5	414	2	Q9JJK8_MOUSE
20	30	8.1	367	2	Q4R250_TETNG
21	19	5.1	337	2	Q5R990_PONPY
22	14	3.8	214	2	Q69YF0_HUMAN
23	14	3.8	700	2	Q9VN23_DROME
24	13	3.5	338	2	Q74426_SCHPO
25	12	3.3	311	2	Q6KJR8_ORYSA
26	12	3.3	379	2	Q21483_CAEEL
27	12	3.3	380	2	Q60Y37_CAEER
28	11	3.0	210	2	Q5TV49_ANOGA
29	11	3.0	278	2	Q7QF68_ANOGA
30	11	3.0	509	2	Q4P7E0_USTWA
31	11	3.0	824	2	Q6ZFB3_ORYSA

32	10	2.7	270	2	Q6ULS3_SOYBN	06ula3 glycine max
33	10	2.7	282	2	Q949L9_BETVU	0949l9 beta vulgar
34	10	2.7	307	2	Q94EN6_SORBI	094en6 sorghum bic
35	10	2.7	311	2	Q5EC57_MAIZE	05ec57 zea mays (m
36	10	2.7	349	2	Q5EUH0_PLAN	05euho gemmata sp.
37	10	2.7	567	2	Q52DZ2_MAGGR	Q52dz2 magnaportha
38	10	2.7	567	2	Q4WMP1_ASPPU	Q4wmp1 aspergillus
39	10	2.7	629	2	Q5AVZ3_EMENI	Q5avz3 aspergillus
40	10	2.7	1158	2	Q7SCY3_NEUCR	07scy3 neurospora
41	10	2.7	1159	2	Q51TP5_MAGGR	051tp5 magnaportha
42	10	2.7	1200	2	Q4IQS5_GIBZE	04iqs5 gibberella
43	9	2.4	97	2	Q5TV47_ANOGA	Q5tv47 anopheles g
44	9	2.4	127	2	Q5TV48_ANOGA	Q5tv48 anopheles g
45	9	2.4	144	2	P79278_PIG	P79278 sus scrofa

ALIGNMENTS

RESULT 1
Q5TQ05_HUMAN
ID Q5TQ05_HUMAN PRELIMINARY; PRT; 369 AA.
AC Q5TQ05;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Protein kinase (PKE).
GN Name=RP11-140A10.1, ORFNames=RP11-140A10.1-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tracey A.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL512622; CA112187.1; -; Genomic DNA.
DR Ensembl; ENSG00000165752; Homo sapiens.
DR GO; GO:0005524; F-ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Kinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
SQ SEQUENCE 369 AA; 42425 MW; 83C54CAF7D792E5 CRC64;

Query Match	100.0%;	Score 369;	DB 2;	Length 369;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 369;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MYAMKYNKQOCIERDEVRN	FRLEILQIEHVFVNLWYSFQDEEDMFVVDLLGGD	60
Db	1	MYAMKYNKQOCIERDEVRN	FRLEILQIEHVFVNLWYSFQDEEDMFVVDLLGGD	60
QY	61	LRVHLQONVQFSDDTVRLVICEMALDYLRLGQHIIHRDVKPNILLDERGHAHLTDFNI	120	
Db	61	LRVHLQONVQFSDDTVRLVICEMALDYLRLGQHIIHRDVKPNILLDERGHAHLTDFNI	120	
QY	121	ATTIKDGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI	180	
Db	121	ATTIKDGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI	180	
QY	181	HSSNAVESLVQLPSTVSQYVPTWSKEMVALLKLLTVNPEHRLSSLDQVQAPALAGVL	240	

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Db 181 HSSNAVESLVQLFSTVSQVPTWNSKEMVALLRKLLTVNPEHRLSSLDQVQAAPALAGVL 240
QY 241 WDHLSEKRVPGFVFNKGRHLCDPTPELEEMILESRPLHKKKRLAKNKSNDNRSSQS 300
Db 241 WDHLSEKRVPGFVFNKGRHLCDPTPELEEMILESRPLHKKKRLAKNKSNDNRSSQS 300
QY 301 ENDYLQDCLDAIQDDFVFNREKLRKSQDLPREPLPAPESRDAAPVEDEAERSALPMCG 360
Db 301 ENDYLQDCLDAIQDDFVFNREKLRKSQDLPREPLPAPESRDAAPVEDEAERSALPMCG 360
QY 361 PICPSAGSG 369
Db 361 PICPSAGSG 369

RESULT 2
Q86UX6_HUMAN
ID Q86UX6_HUMAN PRELIMINARY; PRT; 486 AA.
AC Q86UX6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE PKC protein kinase.
GN Name:STK32C; Synonyms:RP11-140A10.1; ORFNames:RP11-140A10.1-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ma A.-H., Nelson D.A., Xia L., Ravi L., Chen H.-C., Robinson D.R.,
RA Kung H.-J.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Tracey A.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Brown J.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AY098866; AAM21719.1; -; mRNA.
DR EMBL; AL512622; CAI12181.1; -; Genomic DNA.
DR EMBL; AL590105; CAI13011.1; -; Genomic DNA.
DR EMBL; AL590105; CAI12181.1; JOINED; Genomic DNA.
DR EMBL; AL512622; CAI13011.1; JOINED; Genomic DNA.
DR HSSP; P31751; IMRV.
DR Ensembl; ENSG00000165752; Homo sapiens.
DR HGNC; HGNC:21332; STK32C.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004688; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 486 AA; 54994 MW; 38FEFB3863B21F3 CRC64;
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Query Match 100.0%; Score 369; DB 2; Length 486;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MYAMKYNKQOCIERDEVNVPRELEIIQETIEHFLVNLWYSFQDEDMFVVLDLLGSD 60
Db 118 MYAMKYNKQOCIERDEVNVPRELEIIQETIEHFLVNLWYSFQDEDMFVVLDLLGSD 177
QY 61 LRYHLQONVQFSEDVRLVYICEMALALDYLRQCHIHRDVKPDNILLDERGHAHLTDFNI 120
Db 178 LRYHLQONVQFSEDVRLVYICEMALALDYLRQCHIHRDVKPDNILLDERGHAHLTDFNI 237
QY 121 ATIIKDGSRATALAGTKPYMAPEIFHFSFVNGGTGYSFEVDMWSVGMAYELLRGWRPYDI 180
Db 238 ATIIKDGSRATALAGTKPYMAPEIFHFSFVNGGTGYSFEVDMWSVGMAYELLRGWRPYDI 297
QY 181 HSSNAVESLVQLFSTVSQVPTWNSKEMVALLRKLLTVNPEHRLSSLDQVQAAPALAGVL 240
Db 298 HSSNAVESLVQLFSTVSQVPTWNSKEMVALLRKLLTVNPEHRLSSLDQVQAAPALAGVL 357
QY 241 WDHLSEKRVPGFVFNKGRHLCDPTPELEEMILESRPLHKKKRLAKNKSNDNRSSQS 300
Db 358 WDHLSEKRVPGFVFNKGRHLCDPTPELEEMILESRPLHKKKRLAKNKSNDNRSSQS 417
QY 301 ENDYLQDCLDAIQDDFVFNREKLRKSQDLPREPLPAPESRDAAPVEDEAERSALPMCG 360
Db 418 ENDYLQDCLDAIQDDFVFNREKLRKSQDLPREPLPAPESRDAAPVEDEAERSALPMCG 477
QY 361 PICPSAGSG 369
Db 478 PICPSAGSG 486

RESULT 3
Q5TQ04_HUMAN
ID Q5TQ04_HUMAN PRELIMINARY; PRT; 381 AA.
AC Q5TQ04;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Protein kinase (PKE).
GN Name:RP11-140A10.1; ORFNames:RP11-140A10.1-004;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tracey A.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AL512622; CAI12188.1; -; Genomic DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004688; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 381 AA; 43102 MW; 6564FFB4CDF5E333 CRC64;
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Query Match 81.3%; Score 300; DB 2; Length 381;
Best Local Similarity 100.0%; Pred. No. 2e-285;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MYAMKYNKQCCIERDEVNVFRELILQIEIHVFLVNLWYSFQDEDMFVVDLLGGD 60
DB 57 MYAMKYNKQCCIERDEVNVFRELILQIEIHVFLVNLWYSFQDEDMFVVDLLGGD 116
QY 61 LRVHLQONVQFSEDTVRLYICEMALDYLRGQHIHRDVKPDNILLDERGHAHLTD FNI 120
DB 117 LRVHLQONVQFSEDTVRLYICEMALDYLRGQHIHRDVKPDNILLDERGHAHLTD FNI 176
QY 121 ATIIKGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 180
DB 177 ATIIKGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 236
QY 181 HSSNAVESLVQLFSTVSQVPTWSKEMVALLRKLTVNPEHRLSSLDVQAAAPALAGVL 240
DB 237 HSSNAVESLVQLFSTVSQVPTWSKEMVALLRKLTVNPEHRLSSLDVQAAAPALAGVL 296
QY 241 WDHLSEKRVPGFVFNKGRHLCDPTFELEEMILESRLHKKKRLAKNKS RDNRSQS 300
DB 297 WDHLSEKRVPGFVFNKGRHLCDPTFELEEMILESRLHKKKRLAKNKS RDNRSQS 356

RESULT 4
Q86UE1_HUMAN
ID Q86UE1_HUMAN PRELIMINARY; PRT; 369 AA.
AC Q86UE1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE STK32C protein.
GN Name=STK32C;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RG NIH MGC Project;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC045760; AAR45760.1; -; mRNA.
DR HSSP; P31751; 1MRV.
DR Ensembl; ENSG00000165752; Homo sapiens.
DR GO; GO:0005224; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser Thr_pkin_A5.
DR Pfam; PF00069; Pkinase; I.
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DR ProDom; PD000001; Prot kinase; 1.
DR PROSITE; PS0011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS0108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 369 AA; 42395 MW; E152C66B82D78684 CRC64;

Query Match 72.6%; Score 268; DB 2; Length 369;
Best Local Similarity 99.7%; Pred. No. 5.2e-254;
Matches 368; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MYAMKYNKQCCIERDEVNVFRELILQIEIHVFLVNLWYSFQDEDMFVVDLLGGD 60
DB 1 MYAMKYNKQCCIERDEVNVFRELILQIEIHVFLVNLWYSFQDEDMFVVDLLGGD 60
QY 61 LRVHLQONVQFSEDTVRLYICEMALDYLRGQHIHRDVKPDNILLDERGHAHLTD FNI 120
DB 61 LRVHLQONVQFSEDTVRLYICEMALDYLRGQHIHRDVKPDNILLDERGHAHLTD FNI 120
QY 121 ATIIKGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 180
DB 121 ATIIKGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 180
QY 181 HSSNAVESLVQLFSTVSQVPTWSKEMVALLRKLTVNPEHRLSSLDVQAAAPALAGVL 240
DB 181 HSSNAVESLVQLFSTVSQVPTWSKEMVALLRKLTVNPEHRLSSLDVQAAAPALAGVL 240
QY 241 WDHLSEKRVPGFVFNKGRHLCDPTFELEEMILESRLHKKKRLAKNKS RDNRSQS 300
DB 241 WDHLSEKRVPGFVFNKGRHLCDPTFELEEMILESRLHKKKRLAKNKS RDNRSQS 300
QY 301 ENDYLQDCLDALQQDFVFNREKLRKSDQLPREPLPAPESRDAAEVPEDEAERSALPMCG 360
DB 301 ENDYLQDCLDALQQDFVFNREKLRKSDQLPREPLPAPESRDAAEVPEDEAERSALPMCG 360
QY 361 PICPSAGSG 369
DB 361 PICPSAGSG 369

RESULT 5
Q8QZV4_MOUSE
ID Q8QZV4_MOUSE PRELIMINARY; PRT; 488 AA.
AC Q8QZV4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Serine/threonine kinase 32C (Mus musculus adult male corpora
DE quadrigenina cDNA, RIKEN full-length enriched library,
DE Clone:B230385A21 product:hypothetical serine/threonine protein kinase,
DE full insert sequence).
DE Name=Stk32c;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
```

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmeitz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RC Strausberg R.;
RA Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Konno S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuoka H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Koichiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barch G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenfeld C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [5]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gliss C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perle G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Inotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [6]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Inotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated protein.
CC -!- SIMILARITY: belongs to the Ser/Thr protein kinase family.
DR EMBL; BC026457; AAH26457.1; -; mRNA.
DR HSSP; AK046439; BAC32730.1; -; mRNA.
DR MG1; MG1:2385336; Stk32c.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0008468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser Thr pkin AS.
DR InterPro; IPR002290; Ser Thr pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Hypothetical protein; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase;
SQ SEQUENCE 488 AA; 55263 MW; 2B6A927BE687BEF2 CRC64;
Query Match 30.6%; Score 113; DB 2; Length 488;
Best Local Similarity 100.0%; Pred. NO. 1.1e-101;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 111 GHAIHTDFNIATIIKDGERTALACTKPYMAEIPHSFVNGTGTSGFEYDWSVGWYAYE 170
DB 229 GHAIHTDFNIATIIKDGERTALACTKPYMAEIPHSFVNGTGTSGFEYDWSVGWYAYE 288
QY 171 LLRGWRPYDIHSSNAVESLVQLFSTVSVQVPTWSKEMVALLRLKLLTVNPEHR 223

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Db 289 LLRGWRPYDIHSSNAVESLVQLFSTVSQVPTWSKEMVALLKLLTVNPEHR 341
|||||
RESULT 6
Q9JUG4_MOUSE PRELIMINARY; PRT; 488 AA.
AC Q9JUG4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus brain cDNA, clone MNCB-1563, similar to A2750840
DE serine/threonine protein kinase (Mus musculus).
GN Name:Stk32c; Synonyms=Pek;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=C57BL;
RA Osada N., Kusuda J., Tanuma R., Ito A., Hirata M., Sugano S.,
RA Hashimoto K.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AB041542; BAA95027.1; -, mRNA.
DR HSSP; P31751; IMRV.
DR Ensemble; ENSMUSG00000015981; Mus musculus.
DR MGI; MGI:2385336; Stk32c.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR SMART; SM00220; S_TKc_1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 488 AA; 55277 MW; 310483FF69E24E39 CRC64;
Query Match 30.6%; Score 113; DB 2; Length 488;
Best Local Similarity 100.0%; Pred. No. 1.1e-101;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 GHAHLDFNIATIKDGERATALAGTKPYMAPFIHFISFVNGGTGYSFEVDWWSVGVMAYE 170
|||||
DB 229 GHAHLDFNIATIKDGERATALAGTKPYMAPFIHFISFVNGGTGYSFEVDWWSVGVMAYE 288
|||||
QY 171 LLRGWRPYDIHSSNAVESLVQLFSTVSQVPTWSKEMVALLKLLTVNPEHR 223
|||||
DB 289 LLRGWRPYDIHSSNAVESLVQLFSTVSQVPTWSKEMVALLKLLTVNPEHR 341
|||||

RESULT 7
Q9BG74_MACFA PRELIMINARY; PRT; 368 AA.
AC Q9BG74;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecidae; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;

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RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Frontal lobe left;
RA Hashimoto K., Osada N., Hida M., Kusuda J., Sugano S.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB056389; BAB33045.1; -, mRNA.
DR HSSP; P31751; IMRV.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Hypothetical protein; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 368 AA; 42218 MW; 5D7269B32DABCC14 CRC64;
Query Match 21.4%; Score 79; DB 2; Length 368;
Best Local Similarity 100.0%; Pred. No. 2.1e-68;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 253 FVPNGRLHCDPTFELEEMILESRLPKKKRLAKNKRDSRDSQSEN DYLDCLDAI 312
|||||
DB 253 FVPNGRLHCDPTFELEEMILESRLPKKKRLAKNKRDSRDSQSEN DYLDCLDAI 312
|||||
QY 313 QQDFVIFNREKLKRSQDLP 331
|||||
DB 313 QQDFVIFNREKLKRSQDLP 331
|||||

RESULT 8
Q4RN62_TETNG PRELIMINARY; PRT; 441 AA.
AC Q4RN62;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chromosome undetermined SCAF15016, whole genome shotgun sequence.
GN ORFNames=GSTENG00031718001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN NUCLEOTIDE SEQUENCE.
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Athouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poullain J., De Berardinis V.,
RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Farra G., Lardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN NUCLEOTIDE SEQUENCE.
RP Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; CAAE01015016; CAG10170.1; -, Genomic_DNA.

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SQ SEQUENCE 441 AA; 50816 MW; 71C81AC5A8B49B63 CRC64;
Query Match 18.2%; Score 67; DB 2; Length 441;
Best Local Similarity 100.0%; Pred. No. 1.5e-56;
Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYAMKYNKQOCIERDEVRNVRELEILQIEIHVFLVNLWYSFQDEDMFMVVDLLGGD 60
|||||
Db 66 MYAMKYNKQOCIERDEVRNVRELEILQIEIHVFLVNLWYSFQDEDMFMVVDLLGGD 125
|||||

QY 61 LRYHLOQ 67
|||||
Db 126 LRYHLOQ 132

RESULT 9
Q8WU08 HUMAN
ID Q8WU08 HUMAN PRELIMINARY; PRT; 166 AA.
AC Q8WU08;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Serine/threonine kinase 32A.
GN Name=STK32A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feigold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Bladder;
RA Strausberg R.;
CC Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC 1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC021666; AAH21666.1; -; mRNA.
DR HSSP; P21146; LOW.
DR Ensembl; ENSG00000169302; Homo sapiens.
DR HGNC; HGNC:28317; STK32A.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004674; F:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot.kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot.kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
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KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase
SQ SEQUENCE 166 AA; 19792 MW; CDCF94E54C793BA4 CRC64;
Query Match 9.5%; Score 35; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.6e-25;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 FLVNLWYSFQDEDMFMVVDLLGGDLRYHLOQNV 69
|||||
Db 82 FLVNLWYSFQDEDMFMVVDLLGGDLRYHLOQNV 116

RESULT 10
Q6UXH3 HUMAN
ID Q6UXH3 HUMAN PRELIMINARY; PRT; 364 AA.
AC Q6UXH3;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE HSA250839.
GN ORFNames=UNQ3003;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,
RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
RA Wood W.I., Godowski P.J., Gray A.W.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment."
RL Genome Res. 13:2265-2270 (2003).
DR EMBL; AY358353; AAQ88719.1; -; mRNA.
DR HSSP; P05132; IAPW.
DR Ensembl; ENSG00000152953; Homo sapiens.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:000468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot.kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR InterPro; IPR002290; Ser_Thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot.kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
SQ SEQUENCE 364 AA; 42195 MW; FE52D0CB54C7A27C CRC64;
Query Match 9.5%; Score 35; DB 2; Length 364;
Best Local Similarity 100.0%; Pred. No. 3.3e-25;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 FLVNLWYSFQDEDMFMVVDLLGGDLRYHLOQNV 69
|||||
Db 32 FLVNLWYSFQDEDMFMVVDLLGGDLRYHLOQNV 66

RESULT 11
Q7TPQ4_MOUSE
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Q7TP04_MOUSE PRELIMINARY; PRT; 368 AA.
AC Q7TP04;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Stk32a protein.
GN Name=Stk32a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RP TISSUE=Olfactory epithelium;
RG MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.245603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalish D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Olfactory epithelium;
RA Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC055002; AAH55002.1; -; mRNA.
DR HSSP; P31751; IGZK.
DR Ensembl; ENSMUSG0000039954; Mus musculus.
DR MGI; MGI:2442403; Stk32a.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 368 AA; 43213 MW; 0DB7F6977C39BB56 CRC64;

Query Match 9.5%; Score 35; DB 2; Length 368;
Best Local Similarity 100.0%; Pred. No. 3.4e-25;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 FLVNLWYSFQDEDMFVVDLLGGDLRYHLQNV 69
Db 82 FLVNLWYSFQDEDMFVVDLLGGDLRYHLQNV 116

RESULT 12
Q5RA27_PONPY PRELIMINARY; PRT; 396 AA.
AC Q5RA27;

Q7TP04_MOUSE PRELIMINARY; PRT; 368 AA.
AC Q7TP04;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Stk32a protein.
GN Name=Stk32a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RP TISSUE=Olfactory epithelium;
RG MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.245603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalish D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Olfactory epithelium;
RA Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC055002; AAH55002.1; -; mRNA.
DR HSSP; P31751; IGZK.
DR Ensembl; ENSMUSG0000039954; Mus musculus.
DR MGI; MGI:2442403; Stk32a.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 368 AA; 43213 MW; 0DB7F6977C39BB56 CRC64;

Query Match 9.5%; Score 35; DB 2; Length 368;
Best Local Similarity 100.0%; Pred. No. 3.4e-25;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 FLVNLWYSFQDEDMFVVDLLGGDLRYHLQNV 69
Db 82 FLVNLWYSFQDEDMFVVDLLGGDLRYHLQNV 116

RESULT 12
Q5RA27_PONPY PRELIMINARY; PRT; 396 AA.
AC Q5RA27;

Q7TP04_MOUSE PRELIMINARY; PRT; 368 AA.
AC Q7TP04;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Stk32a protein.
GN Name=Stk32a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RP TISSUE=Olfactory epithelium;
RG MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.245603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalish D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Olfactory epithelium;
RA Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC055002; AAH55002.1; -; mRNA.
DR HSSP; P31751; IGZK.
DR Ensembl; ENSMUSG0000039954; Mus musculus.
DR MGI; MGI:2442403; Stk32a.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot kinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 368 AA; 43213 MW; 0DB7F6977C39BB56 CRC64;

Query Match 9.5%; Score 35; DB 2; Length 396;
Best Local Similarity 100.0%; Pred. No. 3.6e-25;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 FLVNLWYSFQDEDMFVVDLLGGDLRYHLQNV 69
Db 82 FLVNLWYSFQDEDMFVVDLLGGDLRYHLQNV 116

RESULT 13
Q6GQ72_XENLA PRELIMINARY; PRT; 396 AA.
AC Q6GQ72;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MGC80293 protein.
GN Name=MGC80293;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RP TISSUE=Ovary;
RG MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630 (2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa K., Iwata M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer."
 RL Genome Res. 10:1757-1771 (2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,
 RA Saito K., Saitoh K., Sakai K., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,
 RA Takagawa A., Takahashi F., Shinagawa A., Shiraki T., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AK036266; BAC29366.1; -; mRNA.
 DR EMBL; AK044599; BAC31302.1; -; mRNA.
 DR EMBL; AK044474; BAC31941.1; -; mRNA.
 DR HSSP; P31751; 1GZK.
 DR Ensembl; ENSMUSG0000039954; Mus musculus.
 DR MGI; MGI:2442403; Stk32a.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004674; F:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR SMART; SM00220; S_TKC_1.
 DR PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
 DR PROSITE; PS00107; PROTEIN KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
 DR ATP-binding; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 398 AA; 4509 MW; 689BCA5B25CF18BB CRC64;
 Query Match 9.5%; Score 35; DB 2; Length 398;
 Best Local Similarity 100.0%; Pred. No. 3.6e-25;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 35 FLVNLWYSFQDEDMFMVVDLLGGDLRYHLQNV 69
 DB 82 FLVNLWYSFQDEDMFMVVDLLGGDLRYHLQNV 116
 RESULT 15
 Q81Y14_HUMAN
 ID Q81Y14_HUMAN PRELIMINARY; PRT; 414 AA.
 AC Q81Y14;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Serine/threonine kinase 32B.
 GN Name=STK32B;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.B., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Maman A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; BC038238; AAH38238.1; -; mRNA.
 DR HSSP; P31751; 1MRV.
 DR Ensembl; ENSG00000152953; Homo sapiens.
 DR HGNC; HGNC:14217; STK32B.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004674; F:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR SMART; SM00220; S_TKC_1.
 DR PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
 DR PROSITE; PS00107; PROTEIN KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
 DR ATP-binding; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 414 AA; 47784 MW; F0E5EE695FA8242F CRC64;
 Query Match 9.5%; Score 35; DB 2; Length 414;
 Best Local Similarity 100.0%; Pred. No. 3.8e-25;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 35 FLVNLWYSFQDEDMFMVVDLLGGDLRYHLQNV 69
 DB 82 FLVNLWYSFQDEDMFMVVDLLGGDLRYHLQNV 116
 Search completed: May 9, 2006, 10:54:39
 Job time : 232 secs

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 9, 2006, 10:48:47 ; Search time 84 Seconds
(without alignments)
1930.128 Million cell updates/sec

Title: US-10-633-631-2
Perfect score: 369
Sequence: 1 MTAMKYNKQCIERDEVN.....EAERSALPMCGIPCPSAGSG 369

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2442881

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*
9: Geneseq2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	369	100.0	369	5	ABB84299 Human ser
2	369	100.0	369	7	ADJ70605 Human hea
3	369	100.0	486	8	ADJ96618 Human YAN
4	369	100.0	486	8	ADK71861 Human kin
5	337	91.3	485	5	AEE24141 Human kin
6	323	87.5	364	5	AAO17708 Human ser
7	300	81.3	375	4	AAE04371 Human kin
8	300	81.3	442	7	ADG74653 Human kin
9	269	72.9	713	5	ABB06090 Human NS
10	268	72.6	419	4	ABE65599 Novel pro
11	268	72.6	419	8	ADI29204 Human MAR
12	268	72.6	425	4	AAM40592 Human pol
13	254	68.8	429	4	AAE71961 Human TGF
14	217	58.8	419	4	AAM38806 Human pol
15	214	58.0	444	6	AAE37974 Human kin
16	209	56.6	488	6	ABO14992 Human NOV
17	113	30.6	384	6	ABU62279 Mouse ser
18	113	30.6	384	9	ADL09166 Mouse ser
19	113	30.6	384	9	ADZ58502 Mouse ser
20	113	30.6	339	5	ABB84300 Murine se
21	113	30.6	488	5	AAO17709 Murine se
22	79	21.4	368	5	ABB84301 Macaque s
23	35	9.5	160	4	AAU87204 Novel cen
24	35	9.5	160	8	ADI54519 Novel hum

25	35	9.5	225	5	AAE14258	Aae14258 Novel hum
26	35	9.5	236	5	AAE14259	Aae14259 Novel hum
27	35	9.5	253	9	AEA20331	Aea20331 Novel hum
28	35	9.5	327	4	AAU03504	Aau03504 Human pro
29	35	9.5	358	7	ADM03989	Adm03989 Human pro
30	35	9.5	364	4	AAU29309	Aau29309 Human PRO
31	35	9.5	364	6	ABU58685	Abu58685 Human PRO
32	35	9.5	364	6	ABU88233	Abu88233 Novel hum
33	35	9.5	364	6	ABU84548	Abu84548 Human sec
34	35	9.5	364	6	ABR66422	AbR66422 Human sec
35	35	9.5	364	6	ABR65812	AbR65812 Human sec
36	35	9.5	364	6	ABU99752	Abu99752 Human sec
37	35	9.5	364	6	ABU82991	Abu82991 Human PRO
38	35	9.5	364	6	ABU90112	Abu90112 Novel hum
39	35	9.5	364	6	ABR68361	AbR68361 Human sec
40	35	9.5	364	6	ABU96414	Abu96414 Novel hum
41	35	9.5	364	6	ABU92845	Abu92845 Human sec
42	35	9.5	364	6	ABO08922	AbO08922 Human sec
43	35	9.5	364	6	ABO02974	AbO02974 Human sec
44	35	9.5	364	6	ABR75128	AbR75128 Human sec
45	35	9.5	364	6	ABR94890	AbR94890 Human sec

ALIGNMENTS

RESULT 1	
ID	ABB84299 standard; protein; 369 AA.
XX	ABB84299;
AC	XX
XX	XX
DT	12-NOV-2002 (first entry)
XX	XX
DE	Human serine/threonine protein kinase subfamily-related protein.
XX	Serine/threonine protein kinase subfamily; chromosome 10; human; enzyme; cytosolic; gene therapy; drug screening; tissue typing; prostate; lung; pharmacogenomic; brain.
KW	XX
KW	Homo sapiens.
XX	XX
OS	XX
FT	Key Location/Qualifiers
FT	Modified-site 42..45
FT	/note="casein kinase II phosphorylation site"
FT	Modified-site 75..77
FT	/note="protein kinase C phosphorylation site"
FT	Region 95..107
FT	/note="serine/threonine protein kinase active signature motif"
FT	Modified-site 152..157
FT	/note="N-myristoylation site"
FT	Region 185..205
FT	/note="helix region"
FT	Modified-site 226..229
FT	/note="casein kinase II phosphorylation site"
FT	Modified-site 245..247
FT	/note="protein kinase C phosphorylation site"
FT	Modified-site 288..291
FT	/note="N-glycosylation site"
FT	Modified-site 298..301
FT	/note="casein kinase II phosphorylation site"
FT	Modified-site 300..303
FT	/note="casein kinase II phosphorylation site"
WO200259288-A2.	
01-AUG-2002.	
15-JAN-2002; 2002WO-US000930.	
23-JAN-2001; 2001US-0263162P.	
29-MAR-2001; 2001US-00819607.	

Db 61 LRYHLQONVQFSDTVRLYICEMALADYLRGQHI IHRDVKPNILDERGHAHLTD FNI 120
Qy 121 ATIIKQGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGMAYELLRGWRPYDI 180
Db 121 ATIIKQGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGMAYELLRGWRPYDI 180
Qy 181 HSSNAVESLVQLFSTVSQVPTWTSKEMVALLKRLTVNPEHRLSSLDQVQAAPALAGVL 240
Db 181 HSSNAVESLVQLFSTVSQVPTWTSKEMVALLKRLTVNPEHRLSSLDQVQAAPALAGVL 240
Qy 241 WDHLSEKRVPGFVFNKGRHLCDPTFELEMILESRPLHKKKRLAKNKRSDNRSSQS 300
Db 241 WDHLSEKRVPGFVFNKGRHLCDPTFELEMILESRPLHKKKRLAKNKRSDNRSSQS 300
Qy 301 ENDYLQDCLDAIQDDFVIFNREKLKRSQDLPREPLPAPESRDAEPVEDEAERSALPMCG 360
Db 301 ENDYLQDCLDAIQDDFVIFNREKLKRSQDLPREPLPAPESRDAEPVEDEAERSALPMCG 360
Qy 361 PICPSAGSG 369
Db 361 PICPSAGSG 369

RESULT 3
ADJ96618
ID ADJ96618 standard; protein; 486 AA.
XX AC ADJ96618;
XX DT 06-MAY-2004 (first entry)
XX DE Human YANK3 protein SeqID 75.
XX KW kinase; human; tyrosine protein kinase; serine/threonine protein kinase;
KW PKK; STK; gene therapy; cancer; immune-related disease;
KW cardiovascular disease; brain; neuronal associated disease; metabolic;
KW inflammatory disorder; cytostatic; neuroprotective; immunomodulator;
KW antiinflammatory; enzyme; YANK3.
XX OS Homo sapiens.
XX 28.
XX PN WO2004006838-A2.
XX PD 22-JAN-2004.
XX PF 15-JUL-2003; 2003WO-US021730.
XX PR 15-JUL-2002; 2002US-0395632P.
XX PA (SUGEN-) SUGEN INC.
XX PI Whyte D, Manning G, Caenepeel S;
XX WPI; 2004-122753/12.
XX DR N-PSDB; ADJ96552.
XX PT New nucleic acid molecule encoding a kinase polypeptide, useful for
PT preparing a composition for treating diseases or disorders, e.g., cancer,
PT or neurological, immunological or inflammatory disorders.
XX PS Claim 1; SEQ ID NO 75; 366pp; English.
XX CC This invention relates to a novel isolated, enriched or purified nucleic
CC acid molecule that encodes a kinase polypeptide. Specifically, it relates
CC to human tyrosine and serine/threonine protein kinases (PK's and STK's),
CC as well as protein kinase-like enzymes. The present invention describes
CC screening methods to identify agonists, antagonists and antibodies that
CC can be used to modulate the activity or function of the mammalian kinase
CC enzymes. As such, these compositions can be used for gene therapy
CC purposes to treat diseases or disorders including cancer, immune-related
CC diseases, cardiovascular disease, brain or neuronal associated disease,
CC metabolic and inflammatory disorders. Accordingly, they exhibit

CC cytotatic, neuroprotective, immunomodulator and antiinflammatory
CC activities. This polypeptide sequence is a human kinase protein sequence
CC of the invention.
XX Sequence 486 AA;
Qy Query Match 100.0%; Score 369; DB 8; Length 486;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MYAMKYNKQOCIERDEVNVREREILQIEIHVFLVNLWYSFQDEDMFMVVDLLGGD 60
Db 118 MYAMKYNKQOCIERDEVNVREREILQIEIHVFLVNLWYSFQDEDMFMVVDLLGGD 177
Qy 61 LRYHLQONVQFSDTVRLYICEMALADYLRGQHI IHRDVKPNILDERGHAHLTD FNI 120
Db 178 LRYHLQONVQFSDTVRLYICEMALADYLRGQHI IHRDVKPNILDERGHAHLTD FNI 237
Qy 121 ATIIKQGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGMAYELLRGWRPYDI 180
Db 238 ATIIKQGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGMAYELLRGWRPYDI 297
Qy 181 HSSNAVESLVQLFSTVSQVPTWTSKEMVALLKRLTVNPEHRLSSLDQVQAAPALAGVL 240
Db 298 HSSNAVESLVQLFSTVSQVPTWTSKEMVALLKRLTVNPEHRLSSLDQVQAAPALAGVL 357
Qy 241 WDHLSEKRVPGFVFNKGRHLCDPTFELEMILESRPLHKKKRLAKNKRSDNRSSQS 300
Db 358 WDHLSEKRVPGFVFNKGRHLCDPTFELEMILESRPLHKKKRLAKNKRSDNRSSQS 417
Qy 301 ENDYLQDCLDAIQDDFVIFNREKLKRSQDLPREPLPAPESRDAEPVEDEAERSALPMCG 360
Db 418 ENDYLQDCLDAIQDDFVIFNREKLKRSQDLPREPLPAPESRDAEPVEDEAERSALPMCG 477
Qy 361 PICPSAGSG 369
Db 478 PICPSAGSG 486

RESULT 4
ADK71861
ID ADK71861 standard; protein; 486 AA.
XX AC ADK71861;
XX DT 20-MAY-2004 (first entry)
XX DE Human kinase and phosphatase KPP-38 protein.
XX KW human; kinase; phosphatase; KPP; cardiovascular; antiarteriosclerotic;
KW hypotensive; vasotropic; antiinflammatory; antiangiinal; anti-HIV;
KW antiallergic; antiasthmatic; immunosuppressive; antithyroid;
KW dermatological; antidiabetic; nephrotropic; antigout; gastrointestinal;
KW neuroprotective; osteopathic; antiarthritic; antitoxic; ophthalmological;
KW antirheumatic; antiparkinsonian; nootropic; anticonvulsant; hepatotrophic;
KW antipsoriatic; haemostatic; cytostatic; antilipaseic; antiparasitic;
KW antihelminic; antibacterial; virucide; protozoacide; fungicide;
KW cardiovascular disease; immune system; neurological; growth; development;
KW cell proliferation; viral; bacterial; fungal; parasitic; protozoan;
KW helminthic infection; transgenic; gene therapy; enzyme;
KW single nucleotide polymorphism; SNP.
XX OS Homo sapiens.
XX PN WO2004018641-A2.
XX PD 04-MAR-2004.
XX PF 25-AUG-2003; 2003WO-US026635.
XX PR 26-AUG-2002; 2002US-0406172P.
XX PR 25-SEP-2002; 2002US-0413910P.
XX PR 27-SEP-2002; 2002US-0414296P.

CC atherosclerosis, multiple sclerosis, psoriasis), disorders affecting
CC growth and development (e.g., arteriosclerosis, cirrhosis, hepatitis),
CC cardiovascular disorder (e.g., hypertension, myocardial infarction,
CC Goodpasture's syndrome), and a lipid disorder (e.g., fatty liver,
CC Gaucher's disease, Niemann-Pick's disease, hypercholesterolemia,
CC hyperlipidaemia, obesity), and for assessing the effects of exogenous
CC compounds. Anti-PKIN antibody is useful in a diagnostic test for a
CC condition or a disease associated with the expression of PKIN in a
CC biological sample. A composition comprising PKIN or an agonist or
CC antagonist of PKIN is useful for treating a disease or condition
CC associated with decreased or increased expression of functional PKIN.
CC PKIN is useful in a number of drug screening techniques and to analyse
CC the proteome of a tissue or cell type. PKIN DNA is useful for creating
CC knockin humanised animals or transgenic animals to model human diseases,
CC and in somatic or germline gene therapy. The present sequence is human
CC PKIN protein
XX
SQ Sequence 485 AA;
Query Match 91.3%; Score 337; DB 5; Length 485;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYAMKYNKQOCIERDEVRNVFRELEILQIEHVLVNLWYSFQDEDMFVVDLLGGD 60
DB 118 MYAMKYNKQOCIERDEVRNVFRELEILQIEHVLVNLWYSFQDEDMFVVDLLGGD 177
QY 61 LRYHLOQNVQSFSDTVRLVICEMALADYLRGQHHIRVDKPNILLDERGHAHLTD FNI 120
DB 178 LRYHLOQNVQSFSDTVRLVICEMALADYLRGQHHIRVDKPNILLDERGHAHLTD FNI 237
QY 121 ATIIKQGERATAGTKPYNAPEIFHSFVNGGTGYSFEVDWWSGVMAVELLGRWPYDI 180
DB 238 ATIIKQGERATAGTKPYNAPEIFHSFVNGGTGYSFEVDWWSGVMAVELLGRWPYDI 297
QY 181 HSSNAVESLVQLFSTVSQVPTWSEKEMVALLRKLTVNPEHRLSSLDVQAAPALAGVL 240
DB 298 HSSNAVESLVQLFSTVSQVPTWSEKEMVALLRKLTVNPEHRLSSLDVQAAPALAGVL 357
QY 241 WDHLSEKRVPEPGVPNKGRLHCDPTFELEEMILESRLHKKKRLAKNKS RDNSSQS 300
DB 358 WDHLSEKRVPEPGVPNKGRLHCDPTFELEEMILESRLHKKKRLAKNKS RDNSSQS 417
QY 301 ENDYLODCLDAIQDQDFVIFNREKLKRSQDLPREPLPA 337
DB 418 ENDYLODCLDAIQDQDFVIFNREKLKRSQDLPREPLPA 454
RESULT 6
ID AAO17708
XX AC AAO17708;
XX DT 20-AUG-2002 (first entry)
XX DE Human serine-threonine protein kinase.
XX KW Human; serine-threonine protein kinase; cancer; diabetes; obesity;
KW central nervous system disorder; inflammation; gene therapy; COPD;
KW neuroprotective; antiparkinsonian; cerebroprotective; cytostatic;
KW antidiabetic; antiallergic; antiasthmatic; antidepressant; anorectic;
KW antiinflammatory; immunomodulator; chronic obstructive pulmonary disease;
KW enzyme.
XX OS Homo sapiens.
XX PN WO200233056-A2.
XX PD 25-APR-2002.
XX PF 15-OCT-2001; 2001WO-EP011892.

PR 16-OCT-2000; 2000US-0240097P.
XX 30-JUL-2001; 2001US-0308096P.
PA (FARB) BAYER AG.
XX Koehler RH;
PI WPI; 2002-435534/46.
DR N-PSDB; AAL46714.
XX New human serine-threonine protein kinase and encoding polynucleotides,
PT useful for diagnosing, treating and preventing central nervous system
PT disorders (e.g. stroke), diabetes, or cancers (e.g. leukemia).
XX Claim 25; Fig 2; 135pp; English.
XX The present invention provides the protein and coding sequences of a
CC human serine-threonine protein kinase. The sequences can be used in the
CC diagnosis, treatment and prevention of cancers (e.g. leukaemia, lymphoma
CC or melanoma), CNS disorders (e.g. Parkinson's disease, stroke, or
CC traumatic brain injury), diabetes, eating disorders (e.g. obesity,
CC anorexia, or cachexia), allergies, anaphylaxis, asthma, inflammation and
CC chronic obstructive pulmonary disease (COPD). The present sequence is the
CC protein of the invention
XX
SQ Sequence 364 AA;
Query Match 87.5%; Score 323; DB 5; Length 364;
Best Local Similarity 100.0%; Pred. No. 2.5e-309;
Matches 323; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYAMKYNKQOCIERDEVRNVFRELEILQIEHVLVNLWYSFQDEDMFVVDLLGGD 60
DB 13 MYAMKYNKQOCIERDEVRNVFRELEILQIEHVLVNLWYSFQDEDMFVVDLLGGD 72
QY 61 LRYHLOQNVQSFSDTVRLVICEMALADYLRGQHHIRVDKPNILLDERGHAHLTD FNI 120
DB 73 LRYHLOQNVQSFSDTVRLVICEMALADYLRGQHHIRVDKPNILLDERGHAHLTD FNI 132
QY 121 ATIIKQGERATAGTKPYNAPEIFHSFVNGGTGYSFEVDWWSGVMAVELLGRWPYDI 180
DB 133 ATIIKQGERATAGTKPYNAPEIFHSFVNGGTGYSFEVDWWSGVMAVELLGRWPYDI 192
QY 181 HSSNAVESLVQLFSTVSQVPTWSEKEMVALLRKLTVNPEHRLSSLDVQAAPALAGVL 240
DB 193 HSSNAVESLVQLFSTVSQVPTWSEKEMVALLRKLTVNPEHRLSSLDVQAAPALAGVL 252
QY 241 WDHLSEKRVPEPGVPNKGRLHCDPTFELEEMILESRLHKKKRLAKNKS RDNSSQS 300
DB 253 WDHLSEKRVPEPGVPNKGRLHCDPTFELEEMILESRLHKKKRLAKNKS RDNSSQS 312
QY 301 ENDYLODCLDAIQDQDFVIFNREK 323
DB 313 ENDYLODCLDAIQDQDFVIFNREK 335
RESULT 7
ID AAE04371
XX AC AAE04371;
XX DT 04-SEP-2001 (first entry)
XX DE Human kinase (PKIN)-12.
XX KW Human kinase; PKIN-12; therapy; immune disorder; Addison's disease; AIDS;
KW acquired immune deficiency syndrome; growth and developmental disorder;
KW arteriosclerosis; mixed connective tissue disease; MCTD; adenocarcinoma;
KW leukaemia; cardiovascular disease; myocardial infarction; hypertension;
KW lipid disorder; cancer; fatty liver; cholestasis; transgenic animal;
KW gene therapy; antiallergic; antiasthmatic; antithyroid; dermatological;
KW antidiabetic; nephrotrophic; antiulcer; antiarthritic; antirheumatic;



Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYAMKYNKQOCIEREVRNVFRELIOIEHVFVNLWYSFQDEDMFMVVDLLGGD 60
 DB 118 MYAMKYNKQOCIEREVRNVFRELIOIEHVFVNLWYSFQDEDMFMVVDLLGGD 177
 QY 61 LRYHLOQNVQFSDTVRLYICEMALDYLRLGQHIIHRDVKPNILLDERGHAHLTDFNI 120
 DB 178 LRYHLOQNVQFSDTVRLYICEMALDYLRLGQHIIHRDVKPNILLDERGHAHLTDFNI 237
 QY 121 ATIIKGERATAGTKPYMAPEIFHSFVNGGTGYSFVDWWSVGMAYELLGWRPYDI 180
 DB 238 ATIIKGERATAGTKPYMAPEIFHSFVNGGTGYSFVDWWSVGMAYELLGWRPYDI 297
 QY 181 HSNNAVESLVQFSTVSQVVPWTSKEMVALLRKLTVNPEHRLSSLDVQVQAPALAGVL 240
 DB 298 HSNNAVESLVQFSTVSQVVPWTSKEMVALLRKLTVNPEHRLSSLDVQVQAPALAGVL 357
 QY 241 WDHLSEKRVPEPGFVPPNKGRLHCDPTFELEEMILESRLPHKKKRLAKNKSNDNRSSQS 300
 DB 358 WDHLSEKRVPEPGFVPPNKGRLHCDPTFELEEMILESRLPHKKKRLAKNKSNDNRSSQS 417

RESULT 9
 ABB06090
 ID ABB06090 standard; protein; 713 AA.
 AC ABB06090;
 XX
 DT 10-MAY-2002 (first entry)
 DE Human NS protein sequence SEQ ID NO:182.
 KW Human; cytostatic; osteopathic; gynaecological; neuroprotective;
 KW antirheumatic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV;
 KW vasotropic; antiarteriosclerotic; antiinflammatory; dermatological;
 KW anorectic; muscular; antinfertility; cardiovascular; anticoagulant;
 KW antifibrinolytic; hypotension; antiasthmatic; immunomodulator; cardiant;
 KW anticonvulsant; antidiabetic; tranquiliser; antidepressant; auroleptic;
 KW gastrointestinal; virucide; antitumor; cerebroprotective; nootropic;
 KW contractive; vaccine; gene therapy; cancer; osteoporosis; dystonia;
 KW endometriosis; degenerative disease; multiple sclerosis; psoriasis;
 KW rheumatoid arthritis; cataract; restenosis; atherosclerosis; glaucoma;
 KW inflammation; skin disorder; obesity; muscular dystrophy; AIDS;
 KW infertility; cardiovascular disease; coagulation disease; hypertension;
 KW ischaemia; asthma; immune disease; epilepsy; angina; neurodegeneration;
 KW diabetes; anxiety; depression; schizophrenia; viral disease; stroke;
 KW gastric ulcer; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200206315-A2.
 XX
 PD 24-JAN-2002.
 XX
 PF 17-JUL-2001; 2001WO-IL000653.
 XX
 PR 18-JUL-2000; 2000IL-0013745.
 PR 15-DEC-2000; 2000IL-00140354.
 XX
 PA (COMP-) COMPUGEN LTD.
 XX
 PI Mintz L, Freilich S, Bernstein J;
 XX
 DR WPI; 2002-155037/20.
 DR N-PSDB; ABL39744.
 XX
 PT One hundred and twenty eight novel nucleic acid sequences, useful for
 PT treating and diagnosing e.g. cancer, asthma and Alzheimer's.
 XX
 PS Claim 6; Page 207-209; 290pp; English.
 XX
 CC ABL39691 to ABL39818 represent novel human nucleic acid sequences

CC encoding the proteins given in ABB06037 to ABB06164. The novel sequences
 CC (NS) can have cytostatic, osteopathic, gynaecological, neuroprotective,
 CC antirheumatic, antiarthritic, antipsoriatic, ophthalmological, virucide,
 CC vasotropic, antiarteriosclerotic, antiinflammatory, dermatological,
 CC anorectic, muscular, anti-HIV, antinfertility, cardiovascular, cardiant,
 CC anticonvulsant, antidiabetic, tranquiliser, antiasthmatic, antitumor,
 CC immunomodulator, anticonvulsant, antidiabetic, cerebroprotective,
 CC antidepressant, gastrointestinal, auroleptic, cerebroprotective,
 CC nootropic and contraceptive activities. The NS can be used in vaccines,
 CC gene therapy and antitense therapy. Nucleic acids, expression vectors and
 CC antibodies from the present invention can be used for treating and
 CC diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative
 CC diseases, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis,
 CC cataracts, restenosis, atherosclerosis, inflammation, skin disorders,
 CC glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascular
 CC disease, coagulation disease, ischaemia, hypertension, asthma, immune
 CC disease, epilepsy, angina, neurodegeneration, diabetes, anxiety,
 CC depression, schizophrenia, viral disease, gastric ulcers, stroke,
 CC Alzheimer's disease and as a contraceptive
 XX
 SQ Sequence 713 AA;

Query Match 72.9%; Score 269; DB 5; Length 713;
 Best Local Similarity 100.0%; Pred. No. 8e-256;
 Matches 269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 EHVFLVNLWYSFQDEDMFMVVDLLGGDLRYHLOQNVQFSDTVRLYICEMALDYLRL 91
 DB 191 EHVFLVNLWYSFQDEDMFMVVDLLGGDLRYHLOQNVQFSDTVRLYICEMALDYLRL 250
 QY 92 GQHIHRDVKPNILLDERGHAHLTDFNIATIIKGERATAGTKPYMAPEIFHSFVNG 151
 DB 251 GQHIHRDVKPNILLDERGHAHLTDFNIATIIKGERATAGTKPYMAPEIFHSFVNG 310
 QY 152 GTGYSFVDWWSVGMAYELLGWRPYDIHSSNAVESLVQFSTVSQVVPWTSKEMVAL 211
 DB 311 GTGYSFVDWWSVGMAYELLGWRPYDIHSSNAVESLVQFSTVSQVVPWTSKEMVAL 370
 QY 212 LRKLTVNPEHRLSSLDVQVQAPALAGVLWDHLSEKRVPEPGFVPPNKGRLHCDPTFELEEM 271
 DB 371 LRKLTVNPEHRLSSLDVQVQAPALAGVLWDHLSEKRVPEPGFVPPNKGRLHCDPTFELEEM 430
 QY 272 ILESRLPHKKKRLAKNKSNDNRSSQS 300
 DB 431 ILESRLPHKKKRLAKNKSNDNRSSQS 459

RESULT 10
 AAB65599
 ID AAB65599 standard; protein; 419 AA.
 XX
 AC AAB65599;
 XX
 DT 27-MAR-2001 (first entry)
 XX
 DE Novel protein kinase, SEQ ID NO: 124.
 XX
 KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
 KW immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic;
 KW dermatological; antidiabetic; antinfertility; gene therapy; vaccine;
 KW immune disorder; cardiovascular disease; neurodegenerative disease;
 KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
 KW inflammatory pelvic disease; multiple sclerosis; psoriasis.
 XX
 OS Homo sapiens.
 XX
 PN WO2000073469-A2.
 XX
 PD 07-DEC-2000.
 XX
 PF 26-MAY-2000; 2000WO-US014842.
 XX
 PR 28-MAY-1999; 99US-0136503P.

XX (SUGE-) SUGEN INC.
XX Plowman GD, Martinez R, Whyte D, Sudersanam S;
XX WPI; 2001-032161/04.
XX N-PSDB; AAF44624.
XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and
PT treating immune-related diseases and disorders, cardiovascular disease,
PT neurodegenerative diseases and/or cancers.
XX Claim 10; Fig 1; 310pp; English.
XX The present sequence is a novel protein kinase. The novel protein kinases
CC and the nucleic acids that encode them may be used in the treatment and
CC diagnosis of diseases associated with inappropriate kinase expression
CC such as immune-related diseases and disorders, cardiovascular disease,
CC neurodegenerative diseases and/or cancers. The nucleic acids and
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays. The kinase polypeptides may be used as antigens in the production
CC of antibodies of kinase expression and activity. Anti-kinase antibodies
CC and kinase antagonists may also be used to down regulate kinase
CC expression and activity. Diseases related to kinase expression and
CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
CC disorders, complications of organ transplantation, myocardial infarction,
CC immune disorders, cardiomyopathies, strokes, renal failure, oxidative-
CC stress related disorders, chronic inflammatory bowel disease, chronic
CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
CC psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive
CC disorders
XX Sequence 419 AA;
XX Query Match 72.6%; Score 268; DB 4; Length 419;
XX Best Local Similarity 99.7%; Pred. No. 4.7e-255;
XX Matches 368; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MYAMKYNKQOCIERDEVNVRNPRELEIQEIEHVFVLNLYWYFQDEDMFMVVDLLGLGD 60
DB 51 MYAMKYNKQOCIERDEVNVRNPRELEIQEIEHVFVLNLYWYFQDEDMFMVVDLLGLGD 110
QY 61 LRYHLQONVQFSEDTRVRLYICEMALDYLRCQHIIHRDVKPDNILLDERGHAHLTDFNI 120
DB 111 LRYHLQONVQFSEDTRVRLYICEMALDYLRCQHIIHRDVKPDNILLDERGHAHLTDFNI 170
QY 121 ATTIKDGGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 180
DB 171 ATTIKDGGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 230
QY 181 HSSNAVESLVQLFSTVSVQVYPTWMSKEMVALLRKLLTVNPEHRLSSLDQVQAAPALAGVL 240
DB 231 HSSNAVESLVQLFSTVSVQVYPTWMSKEMVALLRKLLTVNPEHRLSSLDQVQAAPALAGVL 290
QY 241 WDHLSEKRVPGFVFNKGRHLCDPTFELEEMILESRLPKKKRLAKNKSNDNRSSQS 300
DB 291 WDHLSEKRVPGFVFNKGRHLCDPTFELEEMILESRLPKKKRLAKNKSNDNRSSQS 350
QY 301 ENDYLQDCLDAIQDDFVIFNREKLKESQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
DB 351 ENDYLQDCLDAIQDDFVIFNREKLKESQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 410
QY 361 PICPSAGSG 369
DB 411 PICPSAGSG 419
RESULT 11
AD129204
ID AD129204 standard; protein; 419 AA.
XX
AC AD129204;
XX

DT 22-APR-2004 (first entry)
XX Human MARK3-associated protein #2.
DE
XX
XX Human; antisense gene therapy; MARK3;
KW MAP/microtubule affinity-regulating kinase 3; cancer;
KW Alzheimer's disease; neurodegenerative disorder;
KW hyperproliferative disorder; cytostatic.
XX
OS Homo sapiens.
XX
PN US2003232771-A1.
XX
PD 18-DEC-2003.
XX
PF 17-JUN-2002; 2002US-00174319.
XX
PR 17-JUN-2002; 2002US-00174319.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Ward DT, Freier SM, Dobie KW;
DR WPI; 2004-052188/05.
DR N-PSDB; ADI29322.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
PT microtubule-affinity-regulating kinases (MARK3), useful for modulating
PT expression of MARK3 or for treating cancer or Alzheimer's disease.
XX
PS Disclosure; SEQ ID NO 124; 233pp; English.
XX
XX The invention relates to a compound comprising a sequence comprising 8-80
CC base pairs (bp) targeted to a nucleic acid encoding MARK3
CC (MAP/microtubule affinity-regulating kinase 3), that specifically
CC hybridizes with the nucleic acid encoding MARK3 and inhibits expression
CC of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a
CC composition comprising the compound and a carrier or diluent, inhibiting
CC the expression of MARK3 in cells or tissues, treating an animal having or
CC suspected of having a disease or condition associated with MARK3 and
CC screening for an antisense compound. The antisense oligonucleotide is
CC useful for preparing a composition for treating hyperproliferative
CC disorder, particularly cancer and neurodegenerative diseases e.g.
CC Alzheimer's disease. The present sequence is a MARK3 associated protein
CC included in the figures but not mentioned anywhere else in the
CC specification.
XX
XX Sequence 419 AA;
XX Query Match 72.6%; Score 268; DB 8; Length 419;
XX Best Local Similarity 99.7%; Pred. No. 4.7e-255;
XX Matches 368; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MYAMKYNKQOCIERDEVNVRNPRELEIQEIEHVFVLNLYWYFQDEDMFMVVDLLGLGD 60
DB 51 MYAMKYNKQOCIERDEVNVRNPRELEIQEIEHVFVLNLYWYFQDEDMFMVVDLLGLGD 110
QY 61 LRYHLQONVQFSEDTRVRLYICEMALDYLRCQHIIHRDVKPDNILLDERGHAHLTDFNI 120
DB 111 LRYHLQONVQFSEDTRVRLYICEMALDYLRCQHIIHRDVKPDNILLDERGHAHLTDFNI 170
QY 121 ATTIKDGGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 180
DB 171 ATTIKDGGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 230
QY 181 HSSNAVESLVQLFSTVSVQVYPTWMSKEMVALLRKLLTVNPEHRLSSLDQVQAAPALAGVL 240
DB 231 HSSNAVESLVQLFSTVSVQVYPTWMSKEMVALLRKLLTVNPEHRLSSLDQVQAAPALAGVL 290
QY 241 WDHLSEKRVPGFVFNKGRHLCDPTFELEEMILESRLPKKKRLAKNKSNDNRSSQS 300
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QY 301 ENDYLDCLDAIQDVFVFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
Db |||||
QY 351 ENDYLDCLDAIQDVFVFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 410
Db |||||
QY 361 PICPSAGSG 369
Db |||||
411 PICPSAGSG 419

RESULT 12
AAM40592
ID AAM40592 standard; protein; 425 AA.
XX
AC AAM40592;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 5523.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; Chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
FN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR N-PSDB; AAI59748.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
PT
XX
PS Example 2; SEQ ID NO 5523; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemoractic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemia and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification

XX SQ Sequence 425 AA;
Query Match 72.6%; Score 268; DB 4; Length 425;
Best Local Similarity 99.7%; Pred. No. 4.8e-255;
Matches 368; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MYAMKYMNKQOCIERDEVRNVFRELEILOEIEHVFVLNLMWYSFQDEEDMFVVDLLGGD 60
Db |||||
57 MYAMKYMNKQOCIERDEVRNVFRELEILOEIEHVFVLNLMWYSFQDEEDMFVVDLLGGD 116
QY 61 LRYHLOONVQFSEDTVRLYICEMALDYLRGQHIHRDVKPNILLDERGHAHLDTFNI 120
Db |||||
117 LRYHLOONVQFSEDTVRLYICEMALDYLRGQHIHRDVKPNILLDERGHAHLDTFNI 176
QY 121 ATTIKDGERTALAGTKPYMAPEIFHSFVNGGTGYSFEVDWNSVGMAYELLRGWRPYDI 180
Db |||||
177 ATTIKDGERTALAGTKPYMAPEIFHSFVNGGTGYSFEVDWNSVGMAYELLRGWRPYDI 236
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Db |||||
237 HSSNAVESLVQLFSTVSQVPTWSEKEMVALLRKLTVPNPEHRLSSLDQVQAAPALAGVL 296
QY 241 WDHLSEKRVPEPGVPNKGRLHCDPTFELBEMILESRLHKKKRLAKNKRDRNSRSSQS 300
Db |||||
297 WDHLSEKRVPEPGVPNKGRLHCDPTFELBEMILESRLHKKKRLAKNKRDRNSRSSQS 356
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Db |||||
357 ENDYLDCLDAIQDVFVFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 416
QY 361 PICPSAGSG 369
Db |||||
417 PICPSAGSG 425

RESULT 13
AAB71961
ID AAB71961 standard; protein; 429 AA.
XX
AC AAB71961;
XX
DT 11-MAY-2001 (first entry)
XX
DE Human TGF-beta receptor encoded by cDNA clone HTEMH65.
XX
KW Human; antisclerotic; dermatological; immunosuppressive; cytostatic;
KW antiinflammatory; anti-HIV; immunostimulant; cardiac; vascular;
KW ophthalmological; neuroprotective; nootropic; anticonvulsant; vaccine;
KW antiparkinsonian; antimicrobial; vulnery; gene therapy; infection;
KW transforming growth factor; TGF; TGF-beta receptor; immune disorder;
KW hyperproliferative disorder; cardiovascular disease; angiogenesis;
KW neurological disorder.
XX
OS Homo sapiens.
XX
PN WO200112670-A1.
XX
PD 22-FEB-2001.
XX
PF 10-AUG-2000; 2000WO-US021736.
XX
PR 13-AUG-1999; 99US-0148682P.
PR 20-SEP-1999; 99US-0154887P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Ni J;
XX
DR WPI; 2001-202858/20.
DR N-PSDB; AAF75340.
XX
XX Nucleic acid molecules encoding 12 transforming growth factor-beta
PT

PT receptor polypeptides, useful for preventing, diagnosing and treating
PT e.g. cancers, Parkinson's disease and diabetic retinopathy.
XX
PS Claim 11; Page 299-300; 31pp; English.
XX
CC The present sequence is one of 12 novel human transforming growth factor
CC (TGF)-beta receptor polypeptides. The TGF-beta receptor polynucleotides
CC and polypeptides may be used in the prevention, diagnosis and treatment
CC of diseases associated with inappropriate polypeptide expression. Such
CC diseases include immune disorders (e.g. multiple sclerosis, systemic
CC lupus erythematosus and human immuno-deficiency virus (HIV) infections),
CC hyperproliferative disorders (e.g. cancers and Gaucher's disease),
CC cardiovascular diseases (e.g. Scimitar syndrome, Chaga's cardiomyopathy
CC and coronary arteriosclerosis), angiogenic disorders (e.g. corneal graft
CC neovascularisation and diabetic retinopathy), neurological disorders
CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease)
CC and infectious diseases. The polynucleotides and polypeptides are also
CC useful for promoting wound healing, regeneration and/or chemotaxis. The
CC polynucleotides and their complementary sequences may also be used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar nucleic acid sequences in samples. The polypeptides may be used
CC as antigens in the production of antibodies and in assays to identify
CC modulators of protein expression and activity. The anti-TGF-beta receptor
CC antibodies may be used to down regulate expression and activity and as
CC diagnostic agents for detecting the presence of the polypeptides in
CC samples
XX
SQ Sequence 429 AA;

Query Match 68.8%; Score 254; DB 4; Length 429;
Best Local Similarity 100.0%; Pred. No. 3.1e-241; Indels 0; Gaps 0;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MALADYLRGQHIHRDVKPDNILLDERGHAHLTDENIATIIKDGERTALAGTKPYMAP 60
QY 143 EIFHSFVNGGTGYSFVDWWSVGVMAYELLRGWRPYDIIHSSNAVESLVQLFSTVSQYYP 202
DB 61 EIFHSFVNGGTGYSFVDWWSVGVMAYELLRGWRPYDIIHSSNAVESLVQLFSTVSQYYP 120
QY 203 TWSKEMVALLKLLTVPNHRLLSSLDVQAAPALAGVLDHLSKKRVEPGFVPNKGRLHC 262
DB 121 TWSKEMVALLKLLTVPNHRLLSSLDVQAAPALAGVLDHLSKKRVEPGFVPNKGRLHC 180
QY 263 DPTFELEEMILSRPLHKKKRLAKNKSNDSDSSQSENDYLQDCLDAIQDDFVIFNRE 322
DB 181 DPTFELEEMILSRPLHKKKRLAKNKSNDSDSSQSENDYLQDCLDAIQDDFVIFNRE 240
QY 323 KLKRSQDLPREPLP 336
DB 241 KLKRSQDLPREPLP 254

RESULT 14
AAM38806
ID AAM38806 standard; protein; 419 AA.
XX
AC AAM38806;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 1951.
XX
KW Human; neurotrophic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW leukaemia.
XX
OS Homo sapiens.

PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao Q;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR N-PSDB; AAI57962.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
PS
PS Example 3; SEQ ID NO 1951; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with neurotrophic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 419 AA;

Query Match 58.8%; Score 217; DB 4; Length 419;
Best Local Similarity 100.0%; Pred. No. 9e-205; Indels 0; Gaps 0;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 153 TGYSFEVDWWSVGVMAYELLRGWRPYDIIHSSNAVESLVQLFSTVSQYYPVTSKENVALL 212
DB 203 TGYSFEVDWWSVGVMAYELLRGWRPYDIIHSSNAVESLVQLFSTVSQYYPVTSKENVALL 262
QY 213 RKLLTVPNHRLLSSLDVQAAPALAGVLDHLSKKRVEPGFVPNKGRLHCDDPTFELEEMI 272
DB 263 RKLLTVPNHRLLSSLDVQAAPALAGVLDHLSKKRVEPGFVPNKGRLHCDDPTFELEEMI 322
QY 273 LESRPLHKKKRLAKNKSNDSDSSQSENDYLQDCLDAIQDDFVIFNREKLKRSQDLPR 332
DB 323 LESRPLHKKKRLAKNKSNDSDSSQSENDYLQDCLDAIQDDFVIFNREKLKRSQDLPR 382
QY 333 EPLPAPESDAAEPVEDEAERSALPMCGPICPSAGSG 369
DB 383 EPLPAPESDAAEPVEDEAERSALPMCGPICPSAGSG 419
RESULT 15
AAE37974
ID AAE37974 standard; protein; 444 AA.
XX

AAE37974;
 06-NOV-2003 (first entry)
 Human kinase and phosphatase (KPP-19) protein.
 Human; kinase; phosphatase; KPP; cell proliferative disorder; hepatitis; atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer; psoriasis; thrombocytopenia; developmental disorder; Reiter's syndrome; renal tubular acidosis; anaemia; mental retardation; Alzheimer's disease; neurological disorder; Parkinson's disease; epilepsy; glomerulonephritis; autoimmune disorder; inflammatory disorder; AIDS; Goodpasture's syndrome; acquired immune deficiency syndrome; immunosuppressive; Crohn's disease; neutropenic; transgenic; dermatitis; multiple sclerosis; diabetes mellitus; allergy; gout; Grave's disease; Hashimoto's thyroiditis; bowel syndrome; osteoporosis; rheumatoid arthritis; Sjogren's syndrome; ophthalmological; gene therapy; asthma; anticonvulsant; uropathic; pancreatitis.
 Homo sapiens.
 OS
 XX
 PN W02003050084-A2.
 XX
 XX 19-JUN-2003.
 PD
 XX
 XX 06-DEC-2002; 2002WO-US039126.
 PF
 XX
 XX 07-DEC-2001; 2001US-0340235P.
 PR
 XX 19-DEC-2001; 2001US-0343007P.
 PR
 XX 21-DEC-2001; 2001US-0343546P.
 PR
 XX 04-FEB-2002; 2002US-0354388P.
 PR
 XX 15-FEB-2002; 2002US-0357675P.
 PR
 XX (INCY-) INCYTE GENOMICS INC.
 XX
 XX Kable AE, Chien D, Wilson AD, Swarnakar A, Gervad AE;
 PI Hafalia AJA, Emerling BM, Ramkumar J, Jin P, Griffin JA, Marquis JP;
 PI Baughn MR, Chawla NK, Lehr-Mason PM, Khare R, Lee S, Hawkins PR;
 PI Becha SD, Lee SY, Sprague WW, Zebardjian Y;
 XX
 DR WPI; 2003-532894/50.
 DR N-PSDB; AAD57346.
 XX
 XX New human kinases and phosphatases and polynucleotides, useful for
 PT diagnosing, treating or preventing autoimmune or inflammatory disorders
 PT (e.g. AIDS, allergy or anaemia), multiple sclerosis, osteoarthritis,
 PT cancer or hepatitis.
 XX
 PS Claim 1; Page 224-225; 282pp; English.
 XX
 CC The invention relates to an isolated polypeptide, which is a human kinase
 CC and phosphatase (KPP). KPP agonists and antagonists are useful for
 CC diagnosing, treating or preventing disorders associated with aberrant
 CC expression of KPP, particularly cell proliferative disorders (e.g.
 CC atherosclerosis, arteriosclerosis, cirrhosis, hepatitis, paroxysmal
 CC nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary
 CC thrombocytopenia or cancer), developmental disorders (eg. renal tubular
 CC acidosis, anaemia or mental retardation), neurological disorders (e.g.
 CC Alzheimer's disease, Parkinson's disease or epilepsy), autoimmune/
 CC inflammatory disorders (e.g. AIDS; acquired immune deficiency syndrome,
 CC allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's
 CC disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome,
 CC gout, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome,
 CC multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's
 CC syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral,
 CC bacterial, fungal, parasitic, protozoan or helminthic infections. The KPP
 CC is useful in assessing the effects of exogenous compounds on the
 CC expression of nucleic acids and kinases and phosphatases. KPP gene is
 CC useful in gene therapy and for creating transgenic animals to model human
 CC disease. The present sequence is human KPP protein
 XX
 SQ Sequence 444 AA;

Query Match 58.0%; Score 214; DB 6; Length 444;

Best Local Similarity 100.0%; Pred. No. 8.6e-202;
 Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 118 MYAMKYNKQOCIERDEVRNVFRELEILOEIEHVLNLMWYSFQDEEDMFVVDLLGGD 177
 Qy 61 LRYHLOQNVQFSEDVTVRLVICENALALDYLRGQHIHRDVKPDNILLDERGHAHLTDNI 120
 Db 178 LRYHLOQNVQFSEDVTVRLVICENALALDYLRGQHIHRDVKPDNILLDERGHAHLTDNI 237
 Qy 121 ATTIKGERATAGTKPYMAPBIFHSFVNGGTGYSFEVDWWSVGMAYELLGWRPYDI 180
 Db 238 ATTIKGERATAGTKPYMAPBIFHSFVNGGTGYSFEVDWWSVGMAYELLGWRPYDI 297
 Qy 181 HSSNAVESLVOLFSTVSQVYVPTWSKEMVALLRK 214
 Db 298 HSSNAVESLVOLFSTVSQVYVPTWSKEMVALLRK 331

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GenCore version 5.1.8
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OM protein - protein search, using sw model

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Gapop 60.0 , Gapext 60.0

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Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	369	100.0	369	2	US-09-819-607-2
2	369	100.0	419	2	US-09-799-875-14
3	113	30.6	384	2	US-09-801-876B-6
4	113	30.6	384	2	US-10-254-869-6
5	113	30.6	384	2	US-10-667-442-6
6	113	30.6	399	2	US-09-819-607-4
7	79	21.4	368	2	US-09-819-607-5
8	35	9.5	225	2	US-09-841-683-5
9	35	9.5	225	2	US-10-620-845-5
10	35	9.5	236	2	US-09-841-683-7
11	35	9.5	236	2	US-10-620-845-7
12	35	9.5	396	2	US-09-801-876B-2
13	35	9.5	396	2	US-09-841-683-11
14	35	9.5	396	2	US-10-254-869-2
15	35	9.5	396	2	US-10-667-442-2
16	35	9.5	396	2	US-10-620-845-11
17	35	9.5	403	2	US-09-801-876B-5
18	35	9.5	403	2	US-10-254-869-5
19	35	9.5	403	2	US-10-667-442-5
20	35	9.5	404	2	US-09-801-876B-4
21	35	9.5	404	2	US-10-254-869-4
22	35	9.5	404	2	US-10-667-442-4
23	35	9.5	407	2	US-09-841-683-9
24	35	9.5	407	2	US-10-620-845-9
25	29	7.9	316	2	US-09-801-876B-7
26	29	7.9	316	2	US-10-254-869-7
27	29	7.9	316	2	US-10-667-442-7

28	14	3.8	178	2	US-09-270-767-31704	Sequence 31704, A
29	14	3.8	178	2	US-09-270-767-46921	Sequence 46921, A
30	12	3.3	347	2	US-09-801-876B-8	Sequence 8, Appli
31	12	3.3	347	2	US-10-254-869-8	Sequence 8, Appli
32	12	3.3	347	2	US-10-667-442-8	Sequence 8, Appli
33	9	2.4	128	2	US-09-270-767-33111	Sequence 33111, A
34	9	2.4	128	2	US-09-270-767-48328	Sequence 48328, A
35	9	2.4	378	2	US-09-771-161A-130	Sequence 130, App
36	9	2.4	399	2	US-09-813-818-4	Sequence 4, Appli
37	9	2.4	399	2	US-10-199-333-4	Sequence 3, Appli
38	9	2.4	401	2	US-09-813-818-3	Sequence 3, Appli
39	9	2.4	401	2	US-10-199-333-3	Sequence 2, Appli
40	9	2.4	409	2	US-09-813-818-2	Sequence 3, Appli
41	9	2.4	409	2	US-10-199-333-2	Sequence 2, Appli
42	9	2.4	415	1	US-08-454-097-35	Sequence 35, Appl
43	9	2.4	415	2	US-08-185-359-35	Sequence 35, Appl
44	9	2.4	415	2	US-09-457-040B-22	Sequence 22, Appl
45	9	2.4	415	2	US-09-538-092-1145	Sequence 1145, Ap

ALIGNMENTS

RESULT 1
US-09-819-607-2
; Sequence 2, Application US/09819607
; Patent No. 6686176
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001078
; CURRENT APPLICATION NUMBER: US/09/819,607
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Human
US-09-819-607-2

Query Match	100.0%;	Score 369;	DB 2;	Length 369;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 369;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
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Db	1	MYAMKYNKQCCIERDEVRN	VFRELEIQIEHVFVNLWYSFQDEEDMFVVDLLGGD	60
Qy	61	LYHLOQNVQFSBDTVRLVICEMALDYLRGQHIIHRDVKPNDILLDERGHAHLTDFNI	120	
Db	61	LYHLOQNVQFSBDTVRLVICEMALDYLRGQHIIHRDVKPNDILLDERGHAHLTDFNI	120	
Qy	121	ATTIKDGERATAGTKPYMAPEIFHSFVNGGYSFVDMWVSGVMAYELLGWRPYDI	180	
Db	121	ATTIKDGERATAGTKPYMAPEIFHSFVNGGYSFVDMWVSGVMAYELLGWRPYDI	180	
Qy	181	HSSNAVESLVQLFSTVSQVPTWSKEMVALLKLTVPNPEHRLSSIQDVQAAAPALAGVL	240	
Db	181	HSSNAVESLVQLFSTVSQVPTWSKEMVALLKLTVPNPEHRLSSIQDVQAAAPALAGVL	240	
Qy	241	WDHLSKRVPEPGVPNKGRLHCDPTFELEEMILESPLHKKKRLAKNKSRRDSSQS	300	
Db	241	WDHLSKRVPEPGVPNKGRLHCDPTFELEEMILESPLHKKKRLAKNKSRRDSSQS	300	
Qy	301	ENDYLODCLDAIQDDFVIFNREKLKRSQDLPREPLPAPSRDAAEPVEDEAERSALPMCG	360	
Db	301	ENDYLODCLDAIQDDFVIFNREKLKRSQDLPREPLPAPSRDAAEPVEDEAERSALPMCG	360	
Qy	361	PICPSAGSG	369	

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Db      361 PICPSAGSG 369

RESULT 2
US-09-799-875-14
; Sequence 14, Application US/09799875
; Patent No. 6638721
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 35800/209996
; CURRENT APPLICATION NUMBER: US/09/799, 875
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/182,059
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/659,287
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-875-14

Query Match      100.0%; Score 369; DB 2; Length 419;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MYAMKTMKQOCIERDEVRNVFRELEIQEIEHVFLVNLWYSFQDEEDMFVVVDLLGGD 60
DB      51 MYAMKTMKQOCIERDEVRNVFRELEIQEIEHVFLVNLWYSFQDEEDMFVVVDLLGGD 110
QY      61 LRYHLOONVQFSEDTVRLYICEMALDYLRCQHIIHRDVKPDNILLDERGHAHLTDFNI 120
DB      111 LRYHLOONVQFSEDTVRLYICEMALDYLRCQHIIHRDVKPDNILLDERGHAHLTDFNI 170
QY      121 ATTIKGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 180
DB      171 ATTIKGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 230
QY      181 HSSNAVESLVQLFSTVSQVYPTWSKEMVALLRKLTVNPEHRLSSLDQVQAAPALAGYL 240
DB      231 HSSNAVESLVQLFSTVSQVYPTWSKEMVALLRKLTVNPEHRLSSLDQVQAAPALAGYL 290
QY      241 WHLSEKRVPEPGVPNKGRLHCDPTFELEEMILESRLHKKKRLAKNKS RDNRSRSSQS 300
DB      291 WHLSEKRVPEPGVPNKGRLHCDPTFELEEMILESRLHKKKRLAKNKS RDNRSRSSQS 350
QY      301 ENDYLODCLDAIQODFVIFNREKLKESQDLPREPLPAPESRDAAEVPEDEAERSALPMCG 360
DB      351 ENDYLODCLDAIQODFVIFNREKLKESQDLPREPLPAPESRDAAEVPEDEAERSALPMCG 410
QY      361 PICPSAGSG 369
DB      411 PICPSAGSG 419

RESULT 3
US-09-801-876B-6
; Sequence 6, Application US/09801876B
; Patent No. 6492155
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: THEREOF
; FILE REFERENCE: CL001160
; CURRENT APPLICATION NUMBER: US/09/801,876B
; CURRENT FILING DATE: 2001-03-09

Db      361 PICPSAGSG 369
DB      411 PICPSAGSG 419

Query Match      100.0%; Score 369; DB 2; Length 419;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MYAMKTMKQOCIERDEVRNVFRELEIQEIEHVFLVNLWYSFQDEEDMFVVVDLLGGD 60
DB      51 MYAMKTMKQOCIERDEVRNVFRELEIQEIEHVFLVNLWYSFQDEEDMFVVVDLLGGD 110
QY      61 LRYHLOONVQFSEDTVRLYICEMALDYLRCQHIIHRDVKPDNILLDERGHAHLTDFNI 120
DB      111 LRYHLOONVQFSEDTVRLYICEMALDYLRCQHIIHRDVKPDNILLDERGHAHLTDFNI 170
QY      121 ATTIKGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 180
DB      171 ATTIKGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 230
QY      181 HSSNAVESLVQLFSTVSQVYPTWSKEMVALLRKLTVNPEHRLSSLDQVQAAPALAGYL 240
DB      231 HSSNAVESLVQLFSTVSQVYPTWSKEMVALLRKLTVNPEHRLSSLDQVQAAPALAGYL 290
QY      241 WHLSEKRVPEPGVPNKGRLHCDPTFELEEMILESRLHKKKRLAKNKS RDNRSRSSQS 300
DB      291 WHLSEKRVPEPGVPNKGRLHCDPTFELEEMILESRLHKKKRLAKNKS RDNRSRSSQS 350
QY      301 ENDYLODCLDAIQODFVIFNREKLKESQDLPREPLPAPESRDAAEVPEDEAERSALPMCG 360
DB      351 ENDYLODCLDAIQODFVIFNREKLKESQDLPREPLPAPESRDAAEVPEDEAERSALPMCG 410
QY      361 PICPSAGSG 369
DB      411 PICPSAGSG 419

RESULT 4
US-10-254-869-6
; Sequence 6, Application US/10254869
; Patent No. 6653117
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: THEREOF
; FILE REFERENCE: CL001160DIV
; CURRENT APPLICATION NUMBER: US/10/254,869
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-254-869-6

Query Match      30.6%; Score 113; DB 2; Length 384;
Best Local Similarity 100.0%; Pred. No. 9.6e-100;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      111 GHAHLTDFNIATIIKGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYE 170
DB      153 GHAHLTDFNIATIIKGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYE 212
QY      171 LLRGWRPYDIHSSNAVESLVQLFSTVSQVYPTWSKEMVALLRKLTVNPEHR 223
DB      213 LLRGWRPYDIHSSNAVESLVQLFSTVSQVYPTWSKEMVALLRKLTVNPEHR 265

RESULT 5
US-10-667-442-6
; Sequence 6, Application US/10667442
; Patent No. 6821765
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: THEREOF
; FILE REFERENCE: CL001160DIV II
; CURRENT APPLICATION NUMBER: US/10/667,442
; CURRENT FILING DATE: 2003-09-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-667-442-6

Query Match      30.6%; Score 113; DB 2; Length 384;
Best Local Similarity 100.0%; Pred. No. 9.6e-100;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      111 GHAHLTDFNIATIIKGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYE 170
DB      153 GHAHLTDFNIATIIKGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYE 212
QY      171 LLRGWRPYDIHSSNAVESLVQLFSTVSQVYPTWSKEMVALLRKLTVNPEHR 223
DB      213 LLRGWRPYDIHSSNAVESLVQLFSTVSQVYPTWSKEMVALLRKLTVNPEHR 265

RESULT 6
US-10-667-442-6
; Sequence 6, Application US/10667442
; Patent No. 6821765
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: THEREOF
; FILE REFERENCE: CL001160DIV II
; CURRENT APPLICATION NUMBER: US/10/667,442
; CURRENT FILING DATE: 2003-09-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-667-442-6

Query Match      30.6%; Score 113; DB 2; Length 384;
Best Local Similarity 100.0%; Pred. No. 9.6e-100;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      111 GHAHLTDFNIATIIKGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYE 170
DB      153 GHAHLTDFNIATIIKGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYE 212
QY      171 LLRGWRPYDIHSSNAVESLVQLFSTVSQVYPTWSKEMVALLRKLTVNPEHR 223
DB      213 LLRGWRPYDIHSSNAVESLVQLFSTVSQVYPTWSKEMVALLRKLTVNPEHR 265

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Query Match 30.6%; Score 113; DB 2; Length 384;
Best Local Similarity 100.0%; Pred. No. 9.6e-100; Indels 0; Gaps 0;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 GHAHLDFTFNATIIKQGERATAGTKPYMAPEIFHSFVNGGTGYSPFVDWWSVGMAYE 170
|||||
DB 153 GHAHLDFTFNATIIKQGERATAGTKPYMAPEIFHSFVNGGTGYSPFVDWWSVGMAYE 212
|||||

QY 171 LLRGWRPYDIHSSNAVESLVQLFSTVSQVPTWSEKEMVALLRKLLTVNPEHR 223
|||||
DB 213 LLRGWRPYDIHSSNAVESLVQLFSTVSQVPTWSEKEMVALLRKLLTVNPEHR 265
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RESULT 6
US-09-819-607-4
; Sequence 4, Application US/09819607
; Patent No. 6686176
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001078
; CURRENT APPLICATION NUMBER: US/09/819,607
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-819-607-4

Query Match 30.6%; Score 113; DB 2; Length 399;
Best Local Similarity 100.0%; Pred. No. 9.9e-100; Indels 0; Gaps 0;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 GHAHLDFTFNATIIKQGERATAGTKPYMAPEIFHSFVNGGTGYSPFVDWWSVGMAYE 170
|||||
DB 141 GHAHLDFTFNATIIKQGERATAGTKPYMAPEIFHSFVNGGTGYSPFVDWWSVGMAYE 200
|||||

QY 171 LLRGWRPYDIHSSNAVESLVQLFSTVSQVPTWSEKEMVALLRKLLTVNPEHR 223
|||||
DB 201 LLRGWRPYDIHSSNAVESLVQLFSTVSQVPTWSEKEMVALLRKLLTVNPEHR 253
|||||

RESULT 7
US-09-819-607-5
; Sequence 5, Application US/09819607
; Patent No. 6686176
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001078
; CURRENT APPLICATION NUMBER: US/09/819,607
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-09-819-607-5

Query Match 21.4%; Score 79; DB 2; Length 368;
Best Local Similarity 100.0%; Pred. No. 3.1e-67; Indels 0; Gaps 0;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 253 FVPNKGRHLCDPTFELEMIKSRPLHKKKRLAKNKS RDNSSQSEN DYLODCLDAI 312
|||||

DB 253 FVPNKGRHLCDPTFELEMIKSRPLHKKKRLAKNKS RDNSSQSEN DYLODCLDAI 312

QY 313 QQDFVIFNREKLRKSQDLP 331
|||||
DB 313 QQDFVIFNREKLRKSQDLP 331
|||||

RESULT 8
US-09-841-683-5
; Sequence 5, Application US/09841683
; Patent No. 6617147
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/09/841,683
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 225
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-841-683-5

Query Match 9.5%; Score 35; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 2.5e-25; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 FLVNLWYSQDEEDMFVVDLLGGDLRYHLQONV 69
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DB 82 FLVNLWYSQDEEDMFVVDLLGGDLRYHLQONV 116
|||||

RESULT 9
US-10-620-845-5
; Sequence 5, Application US/10620845
; Patent No. 6908758
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. 6908758el Human Kinase Proteins and Polynucleotides Encoding
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/10/620,845
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/841,683
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 225
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-620-845-5

Query Match 9.5%; Score 35; DB 2; Length 225;


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RESULT 14
US-10-254-869-2
; Sequence 2, Application US/10254869
; Patent No. 6653117
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160DIV
; CURRENT APPLICATION NUMBER: US/10/254,869
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Human
US-10-254-869-2

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Query Match          9.5%; Score 35; DB 2; Length 396;
Best Local Similarity 100.0%; Pred. No. 4.2e-25;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 FLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNV 69
Db 82 FLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNV 116

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RESULT 15
US-10-667-442-2
; Sequence 2, Application US/10667442
; Patent No. 6821765
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160DIV II
; CURRENT APPLICATION NUMBER: US/10/667,442
; CURRENT FILING DATE: 2003-09-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-667-442-2

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Query Match          9.5%; Score 35; DB 2; Length 396;
Best Local Similarity 100.0%; Pred. No. 4.2e-25;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 FLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNV 69
Db 82 FLVNLWYSFQDEEDMFVVDLLGGDLRYHLQNV 116

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OM protein - protein search, using sw model

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(without alignments)
3146.511 Million cell updates/sec

Title: US-10-633-631-2
Perfect score: 369
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	369	100.0	369	3	US-09-819-607-2
2	369	100.0	369	4	US-10-074-978A-155
3	369	100.0	369	4	US-10-633-631-2
4	369	100.0	369	4	US-10-408-765A-2411
5	369	100.0	419	3	US-09-799-875-14
6	369	100.0	419	4	US-10-303-664A-6
7	369	100.0	419	4	US-10-649-156-14
8	369	100.0	486	4	US-10-618-941-75
9	337	91.3	485	4	US-10-415-011-12
10	300	81.3	375	4	US-10-168-582-12
11	209	56.6	255	4	US-10-074-978A-161
12	209	56.6	258	4	US-10-074-978A-159
13	209	56.6	288	4	US-10-074-978A-18
14	191	51.8	215	4	US-10-074-978A-163
15	113	30.6	384	3	US-09-801-876B-6
16	113	30.6	384	4	US-10-254-869-6
17	113	30.6	384	4	US-10-667-442-6
18	113	30.6	384	5	US-10-962-625-6
19	113	30.6	399	3	US-09-819-607-4
20	113	30.6	399	4	US-10-633-631-4
21	113	30.6	488	4	US-10-074-978A-154
22	79	21.4	368	3	US-09-819-607-5
23	79	21.4	368	4	US-10-074-978A-156
24	79	21.4	368	4	US-10-633-631-5
25	35	9.5	160	3	US-09-764-875-722
26	35	9.5	225	3	US-09-841-683-5
27	35	9.5	225	4	US-10-620-845-5

ALIGNMENTS

RESULT 1

US-09-819-607-2
; Sequence 2, Application US/09819607
; Publication NO. US2003002337A1
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001078
; CURRENT APPLICATION NUMBER: US/09/819,607
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Human
US-09-819-607-2

Query Match	100.0%;	Score 369;	DB 3;	Length 369;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 369;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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DB	1	MYAMKYNKQOCIERDEVNRVNFRELEIQEIEHVFVLNWLWYSFQDESDMMVVDLLLGGD	60	
QY	61	LYRHLQONVQFSEDTVRLYICEMALADYLRGQHIHRDVKPDNILLDERGHAHLTDFNI	120	
DB	61	LYRHLQONVQFSEDTVRLYICEMALADYLRGQHIHRDVKPDNILLDERGHAHLTDFNI	120	
QY	121	ATIIKDGERTALAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI	180	
DB	121	ATIIKDGERTALAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI	180	
QY	181	HSSNAVESLVQLFSTVSVQVYPTWKSVMALLRKLITVNPHEHRLSSLDQVQAAPALAGVL	240	
DB	181	HSSNAVESLVQLFSTVSVQVYPTWKSVMALLRKLITVNPHEHRLSSLDQVQAAPALAGVL	240	
QY	241	WDHLSEKRVPGFVFNKGRGLHCDPTFELEEMTILSRPLHKKKRLAKNKRSDNRSDSSQS	300	
DB	241	WDHLSEKRVPGFVFNKGRGLHCDPTFELEEMTILSRPLHKKKRLAKNKRSDNRSDSSQS	300	
QY	301	ENDYLDQCLDAIQQDFVIFNRKLRKSRQDLPREPAPESRDAAAEPEVEAERSALPMCG	360	
DB	301	ENDYLDQCLDAIQQDFVIFNRKLRKSRQDLPREPAPESRDAAAEPEVEAERSALPMCG	360	
QY	361	PICPSAGSG 369		

Db	361	PICPSAGSG	369	
RESULT 2				
US-10-074-978A-155				
; Sequence 155, Application US/10074978A				
; Publication No. US20040010119A1				
; GENERAL INFORMATION:				
; APPLICANT: Leite, Mario				
; APPLICANT: Spytek, Kimberly A				
; APPLICANT: Guo, Xiaojia (Saaha)				
; APPLICANT: Fernandes, Elma				
; APPLICANT: Li, Li				
; APPLICANT: Kekuda, Ramesh				
; APPLICANT: Liu, Xiahong				
; APPLICANT: Caeman, Stacie				
; APPLICANT: Boldog, Ferenc				
; APPLICANT: Patturajan, Meera				
; APPLICANT: Blalock, Angela				
; APPLICANT: Ballinger, Robert				
; APPLICANT: Vernet, Corine				
; APPLICANT: Tchernev, Velizar T				
; APPLICANT: Malyankar, Uriel M				
; APPLICANT: Gusev, Vladimir				
; APPLICANT: Rastelli, Luca				
; APPLICANT: Mezes, Peter S				
; APPLICANT: Ellerman, Karen				
; APPLICANT: Heyes, Melvin P				
; APPLICANT: Herrman, John				
; APPLICANT: Pena, Carol E A				
; APPLICANT: Shinkets, Richard A				
; APPLICANT: Taupier Jr, Raymond J				
; APPLICANT: Moore, No. US20040010119A11e				
; APPLICANT: Sheno, Suresh				
; APPLICANT: Edinger, Shlomit				
; APPLICANT: Gunther, Erik				
; APPLICANT: Stone, Dave				
; APPLICANT: Millet, Isabelle				
; APPLICANT: Peyman, John				
; APPLICANT: Smithson, Glenda				
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME				
; FILE REFERENCE: 21402-269				
; CURRENT APPLICATION NUMBER: US/10/074,978A				
; CURRENT FILING DATE: 2003-01-07				
; PRIOR APPLICATION NUMBER: 60/268,221				
; PRIOR FILING DATE: 2001-02-12				
; PRIOR APPLICATION NUMBER: 60/335,109				
; PRIOR FILING DATE: 2001-10-31				
; PRIOR APPLICATION NUMBER: 60/312,284				
; PRIOR FILING DATE: 2001-08-14				
; PRIOR APPLICATION NUMBER: 60/268,496				
; PRIOR FILING DATE: 2001-02-13				
; PRIOR APPLICATION NUMBER: 60/276,703				
; PRIOR FILING DATE: 2001-03-16				
; PRIOR APPLICATION NUMBER: 60/330,293				
; PRIOR FILING DATE: 2001-10-18				
; PRIOR APPLICATION NUMBER: 60/322,127				
; PRIOR FILING DATE: 2001-11-21				
; PRIOR APPLICATION NUMBER: 60/280,899				
; PRIOR FILING DATE: 2001-04-02				
; PRIOR APPLICATION NUMBER: 60/310,797				
; PRIOR FILING DATE: 2001-08-08				
; PRIOR APPLICATION NUMBER: 60/268,646				
; PRIOR FILING DATE: 2001-02-14				
; Remaining Prior Application data removed - See File Wrapper or PALM.				
; NUMBER OF SEQ ID NOS: 547				
; SOFTWARE: PatentIn Ver. 2.1				
; SEQ ID NO 155				
; LENGTH: 369				
; TYPE: PRT				
; ORGANISM: Homo sapiens				
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Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
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QY	61	LRYHLQONVQFSEDTVRLYICEMALALDYLRGQHIHRDVKPDNILLDERGHAHLTDFNI	120	
Db	61	LRYHLQONVQFSEDTVRLYICEMALALDYLRGQHIHRDVKPDNILLDERGHAHLTDFNI	120	
QY	121	ATIIKDGGERATAGTKPYMAPEIFHFSFVNGGTGYSFEVDWWSVGMAYELLRGWRPYDI	180	
Db	121	ATIIKDGGERATAGTKPYMAPEIFHFSFVNGGTGYSFEVDWWSVGMAYELLRGWRPYDI	180	
QY	181	HSSNAVESLVQLFSTVSQYVPTWSKEMVALLRKLLTVNPEHRLSSLODQVQAAPALAGVL	240	
Db	181	HSSNAVESLVQLFSTVSQYVPTWSKEMVALLRKLLTVNPEHRLSSLODQVQAAPALAGVL	240	

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Qy 241 WDHLSEKRVPGVPVNGKRLHCDPTFELEEMILESRLPHKKKRLAKNKSNDNRSSQS 300
Db 241 WDHLSEKRVPGVPVNGKRLHCDPTFELEEMILESRLPHKKKRLAKNKSNDNRSSQS 300
Qy 301 ENDYLODCLDAIQODFVFNREKLKRSQDLPREPLPAPSRDAAEPVEAEERSALPMCG 360
Db 301 ENDYLODCLDAIQODFVFNREKLKRSQDLPREPLPAPSRDAAEPVEAEERSALPMCG 360
Qy 361 PICPSAGSG 369
Db 361 PICPSAGSG 369

RESULT 4
US-10-408-765A-2411
; Sequence 2411, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Warnock, Dale E.
; APPLICANT: Glenn, Gary M.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660888.465
; CURRENT APPLICATION NUMBER: US/10/408, 765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2411
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2411

Query Match 100.0%; Score 369; DB 4; Length 369;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYAMKTMNKQCCIERDEVRNFRLEILQIEHVFVNLWYSFQDEDMFMVVDLLGGD 60
Db 1 MYAMKTMNKQCCIERDEVRNFRLEILQIEHVFVNLWYSFQDEDMFMVVDLLGGD 60
Qy 61 LRYHLQONQVFSQDVTVRLYICEMALDYLRGQHIHRDVKPDNILLDERGHAHLTDFNI 120
Db 61 LRYHLQONQVFSQDVTVRLYICEMALDYLRGQHIHRDVKPDNILLDERGHAHLTDFNI 120
Qy 121 ATTIKDGERTALAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 180
Db 121 ATTIKDGERTALAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 180
Qy 181 HSSNAVESLVQFSTVSQVPTWSEKEMVALLRKLTVNPEHRLSSLDVQVQAPALAGVL 240
Db 181 HSSNAVESLVQFSTVSQVPTWSEKEMVALLRKLTVNPEHRLSSLDVQVQAPALAGVL 240
Qy 241 WDHLSEKRVPGVPVNGKRLHCDPTFELEEMILESRLPHKKKRLAKNKSNDNRSSQS 300
Db 241 WDHLSEKRVPGVPVNGKRLHCDPTFELEEMILESRLPHKKKRLAKNKSNDNRSSQS 300
Qy 301 ENDYLODCLDAIQODFVFNREKLKRSQDLPREPLPAPSRDAAEPVEAEERSALPMCG 360
Db 301 ENDYLODCLDAIQODFVFNREKLKRSQDLPREPLPAPSRDAAEPVEAEERSALPMCG 360
Qy 361 PICPSAGSG 369
Db 361 PICPSAGSG 369

RESULT 5
US-09-799-875-14
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; Sequence 14, Application US/09799875
; Patent No. US20020034780A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: No. US20020034780A1el Human Protein Kinases and Uses
; FILE REFERENCE: 35800/209996
; CURRENT APPLICATION NUMBER: US/09/799,875
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/182,059
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/659,287
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-875-14

Query Match 100.0%; Score 369; DB 3; Length 419;
Best Local Similarity 100.0%; Pred. No. 0;
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Db 51 MYAMKTMNKQCCIERDEVRNFRLEILQIEHVFVNLWYSFQDEDMFMVVDLLGGD 110
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Db 111 LRYHLQONQVFSQDVTVRLYICEMALDYLRGQHIHRDVKPDNILLDERGHAHLTDFNI 170
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Db 171 ATTIKDGERTALAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 230
Qy 181 HSSNAVESLVQFSTVSQVPTWSEKEMVALLRKLTVNPEHRLSSLDVQVQAPALAGVL 240
Db 231 HSSNAVESLVQFSTVSQVPTWSEKEMVALLRKLTVNPEHRLSSLDVQVQAPALAGVL 290
Qy 241 WDHLSEKRVPGVPVNGKRLHCDPTFELEEMILESRLPHKKKRLAKNKSNDNRSSQS 300
Db 291 WDHLSEKRVPGVPVNGKRLHCDPTFELEEMILESRLPHKKKRLAKNKSNDNRSSQS 350
Qy 301 ENDYLODCLDAIQODFVFNREKLKRSQDLPREPLPAPSRDAAEPVEAEERSALPMCG 360
Db 351 ENDYLODCLDAIQODFVFNREKLKRSQDLPREPLPAPSRDAAEPVEAEERSALPMCG 410
Qy 361 PICPSAGSG 369
Db 411 PICPSAGSG 419

RESULT 6
US-10-303-664A-6
; Sequence 6, Application US/10303664A
; Publication No. US20030153018A1
; GENERAL INFORMATION:
; APPLICANT: Hunter, John Joseph
; APPLICANT: Williamson, Mark W.
; APPLICANT: Macbeth, Kyle J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CANCER USING 2192, 2193, 6568, 8895, 9138, 9217, 9609,
; TITLE OF INVENTION: 9857, 9882, 10025, 20657, 21163, 25848, 25968, 32603, 32670,
; TITLE OF INVENTION: 33794, 54476 and 94710
; FILE REFERENCE: MPI2001-290F3R(M)
; CURRENT APPLICATION NUMBER: US/10/303,664A
; CURRENT FILING DATE: 2002-11-25
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; NUMBER OF SEQ ID NOS: 57															
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; SEQ ID NO 6															
; LENGTH: 419															
; TYPE: PRT															
; ORGANISM: Homo sapiens															
US-10-303-664A-6															
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Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;															
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Db	51	MYAMKYNKQOCIERDEVNVRFELEIQEIEHVFVNLWYSFQDEEDMFVVDLLGGD	110												
QY	61	LRYHLQONVQFSEDTVRLYICEMALADYLRGQHIHRDVKPDNILLDERGHAHLTDFNI	120												
Db	111	LRYHLQONVQFSEDTVRLYICEMALADYLRGQHIHRDVKPDNILLDERGHAHLTDFNI	170												
QY	121	ATIIKDGERTALAGTKPYMAPEIFHFSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI	180												
Db	171	ATIIKDGERTALAGTKPYMAPEIFHFSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI	230												
QY	181	HSSNAVESLVQFSTVSQVYPTWSKEMVALLRKLLTVNPEHRLSSLODQVQAAPALAGVL	240												
Db	231	HSSNAVESLVQFSTVSQVYPTWSKEMVALLRKLLTVNPEHRLSSLODQVQAAPALAGVL	290												
QY	241	WDHLSEKRVPGFVFNKGRHLHCDPTFELEEMILESRLPKKKKRLAKNKSRRNDRSSQS	300												
Db	291	WDHLSEKRVPGFVFNKGRHLHCDPTFELEEMILESRLPKKKKRLAKNKSRRNDRSSQS	350												
QY	301	ENDYLODCLDAIQODFVIFNREKLKRSQDLPRELPAPESRDAAEPVEDEAERSALPMCG	360												
Db	351	ENDYLODCLDAIQODFVIFNREKLKRSQDLPRELPAPESRDAAEPVEDEAERSALPMCG	410												
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Db	411	PICPSAGSG 419													
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; Sequence 14, Application US/10649156															
; Publication No. US20040038346A1															
; GENERAL INFORMATION:															
; APPLICANT: Meyers, Rachel															
; APPLICANT: Kapeller-Libermann, Rosana															
; APPLICANT: Williamson, Mark															
; TITLE OF INVENTION: No. US20040038346A1el Human Protein Kinases and Uses															
; FILE REFERENCE: 35800/209996															
; CURRENT FILING DATE: 2003-08-27															
; PRIOR FILING DATE: 2001-03-06															
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QY 301 ENDYLDQCLDAIQDVFVFNREKLSQDLPREPLPAPESRDAAEFVEDEAERSALPMCG 360
Db 418 ENDYLDQCLDAIQDVFVFNREKLSQDLPREPLPAPESRDAAEFVEDEAERSALPMCG 477
QY 361 PICPSAGSG 369
Db 478 PICPSAGSG 486

RESULT 9
US-10-415-011-12
; Sequence 12, Application US/10415011
; Publication No. US20040053394A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION
; APPLICANT: GURURAJAN, Rajagopal
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: XU, Yuming
; APPLICANT: ARVIZU, Chandra S.
; APPLICANT: YAO, Monique G.
; APPLICANT: RAMKOMAR, Jayalaxmi
; APPLICANT: DING, Li
; APPLICANT: TANG, Y. Tom
; APPLICANT: HAFALIA, April J.A.
; APPLICANT: NGUYEN, Dannie B.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: LU, Yan
; APPLICANT: YUE, Henry
; APPLICANT: BURFORD, Neil
; APPLICANT: BANDMAN, Olga
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: LAL, Preeti G.
; APPLICANT: RECIPON, Shirley A.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: BOROMSKY, Mark L.
; APPLICANT: THORNTON, Michael B.
; APPLICANT: SWARNAKER, Anita
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: KHAN, Farrah A.
; APPLICANT: ISON, Craig H.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0262 USN
; CURRENT APPLICATION NUMBER: US/10/415,011
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: PCT/US01/47728
; PRIOR FILING DATE: 2001-10-20
; PRIOR APPLICATION NUMBER: US 60/242,410
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/244,068
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/245,708
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/247,672
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/249,565
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: US 60/252,730
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/250,807
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PERL Program
; SEQ ID NO 12
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040053394A1 7473788CD1
US-10-415-011-12

Query Match 91.3%; Score 337; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.4e-307;
Matches 337; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYAMKYNKQOCIERDEVNVPRELEILQIEIHVFLVNLWYSFQDEEDMFVVDDLGGD 60
Db 118 MYAMKYNKQOCIERDEVNVPRELEILQIEIHVFLVNLWYSFQDEEDMFVVDDLGGD 177
QY 61 LRYHLQONVQFSEDVRLVICEMALADYLRGQHIIHRDVKPDNILLDRGHAHLTDENI 120
Db 178 LRYHLQONVQFSEDVRLVICEMALADYLRGQHIIHRDVKPDNILLDRGHAHLTDENI 237
QY 121 ATIIKDGERTALAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGYMAYELLRGWRPYDI 180
Db 238 ATIIKDGERTALAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGYMAYELLRGWRPYDI 297
QY 181 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLDQVQAAPALAGVL 240
Db 298 HSSNAVESLVQLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLDQVQAAPALAGVL 357
QY 241 WDHLSEKRVPGFVFNKGRGLHCDPTFELEEMILESRLPHKKKRLAKNKSNDNRSSQS 300
Db 358 WDHLSEKRVPGFVFNKGRGLHCDPTFELEEMILESRLPHKKKRLAKNKSNDNRSSQS 417
QY 301 ENDYLDQCLDAIQDVFVFNREKLSQDLPREPLPA 337
Db 418 ENDYLDQCLDAIQDVFVFNREKLSQDLPREPLPA 454
RESULT 10
US-10-168-582-12
; Sequence 12, Application US/10168582
; Publication No. US20040058426A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YANG, Junming
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: BURFORD, Neil
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: REDDY, Roopa
; APPLICANT: YUE, Henry
; APPLICANT: YAO, Monique G.
; APPLICANT: LAL, Preeti
; APPLICANT: KAHN, Farrah A.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0002 PCT
; CURRENT APPLICATION NUMBER: US/10/168,582
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 60/172,066; 60/176,107; 60/176,107; 60/177,731
; PRIOR FILING DATE: 1999-12-23; 2000-01-14; 2000-01-14; 2000-01-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 12
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040058426A1 3244919CD1
US-10-168-582-12
Query Match 81.3%; Score 300; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.1e-272;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYAMKYNKQOCIERDEVNVPRELEILQIEIHVFLVNLWYSFQDEEDMFVVDDLGGD 60
Db 51 MYAMKYNKQOCIERDEVNVPRELEILQIEIHVFLVNLWYSFQDEEDMFVVDDLGGD 110
QY 61 LRYHLQONVQFSEDVRLVICEMALADYLRGQHIIHRDVKPDNILLDRGHAHLTDENI 120

Db 111 LRYHLQNNQVQSEDVTRLVYICEMALDYLRCQHIIHRDVKPDNILLDRGHAHLTDFNI 170
QY 121 ATIIKGERATAGTKPYMAPEIFHFSFVNGGTGYSFEVDWWSVGVMAVELLRGWRPYDI 180
Db 171 ATIIKGERATAGTKPYMAPEIFHFSFVNGGTGYSFEVDWWSVGVMAVELLRGWRPYDI 230
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Db 231 HSSNAVESLVQLFSTVSVQVPTWSKEMVALLRKLTLTVNPEHRLSSLODVQAAPALAGVL 290
QY 241 WDHLSEKRVPGFVNPKNRGLHCDPTPELEEMILESRLHKKKRLAKNKSRRNSRDSOS 300
Db 291 WDHLSEKRVPGFVNPKNRGLHCDPTPELEEMILESRLHKKKRLAKNKSRRNSRDSOS 350

RESULT 11

US-10-074-978A-161
; Sequence 161, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
; APPLICANT: Leite, Mario
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Fernandes, Elma
; APPLICANT: Li, Li
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Liu, Xiahong
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Patturajan, Meera
; APPLICANT: Blalock, Angela
; APPLICANT: Ballinger, Robert
; APPLICANT: Vernet, Corine
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter S
; APPLICANT: Ellerman, Karen
; APPLICANT: Heyes, Melvin P
; APPLICANT: Herrman, John
; APPLICANT: Pena, Carol E A
; APPLICANT: Shinkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Moore, No. US20040010119A1lle
; APPLICANT: Sheno, Suresh
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, Dave
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glenna
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-269
; CURRENT APPLICATION NUMBER: US/10/074,978A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: 60/268,221
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/335,109
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/312,284
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/268,496
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/276,703
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/330,293
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/322,127
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/280,899
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/310,797

; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/268,646
; PRIOR FILING DATE: 2001-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 161
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-074-978A-161

Query Match 56.6%; Score 209; DB 4; Length 255;
Best Local Similarity 100.0%; Pred. No. 3.2e-187; Indels 0; Gaps 0;
Matches 209; Conservative 0; Mismatches 0;

QY 1 MYAMKYNKQOCIERDEVNVPRELEILQIEIHFVFLVNLWYSFQDEEDMFVVVDLILGGD 60
Db 27 MYAMKYNKQOCIERDEVNVPRELEILQIEIHFVFLVNLWYSFQDEEDMFVVVDLILGGD 86
QY 61 LRYHLQNNQVQSEDVTRLVYICEMALDYLRCQHIIHRDVKPDNILLDRGHAHLTDFNI 120
Db 87 LRYHLQNNQVQSEDVTRLVYICEMALDYLRCQHIIHRDVKPDNILLDRGHAHLTDFNI 146
QY 121 ATIIKGERATAGTKPYMAPEIFHFSFVNGGTGYSFEVDWWSVGVMAVELLRGWRPYDI 180
Db 147 ATIIKGERATAGTKPYMAPEIFHFSFVNGGTGYSFEVDWWSVGVMAVELLRGWRPYDI 206
QY 181 HSSNAVESLVQLFSTVSVQVPTWSKEMV 209
Db 207 HSSNAVESLVQLFSTVSVQVPTWSKEMV 235

RESULT 12

US-10-074-978A-159
; Sequence 159, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
; APPLICANT: Leite, Mario
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Fernandes, Elma
; APPLICANT: Li, Li
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Liu, Xiahong
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Patturajan, Meera
; APPLICANT: Blalock, Angela
; APPLICANT: Ballinger, Robert
; APPLICANT: Vernet, Corine
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter S
; APPLICANT: Ellerman, Karen
; APPLICANT: Heyes, Melvin P
; APPLICANT: Herrman, John
; APPLICANT: Pena, Carol E A
; APPLICANT: Shinkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Moore, No. US20040010119A1lle
; APPLICANT: Sheno, Suresh
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, Dave
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glenna
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-269
; CURRENT APPLICATION NUMBER: US/10/074,978A

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; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: 60/268,221
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/335,109
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/312,284
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/268,496
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/276,703
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/330,293
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/322,127
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/280,899
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/310,797
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/268,646
; PRIOR FILING DATE: 2001-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 159
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-074-978A-159

Query Match          56.6%; Score 209; DB 4; Length 258;
Best Local Similarity 100.0%; Pred. No. 3.2e-187;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYAMKMNKQOCIERDEVNVPRELEIQEIEHVFVLNLYWYFQDEDMFMVVDLLGGD 60
DB 27 MYAMKMNKQOCIERDEVNVPRELEIQEIEHVFVLNLYWYFQDEDMFMVVDLLGGD 86
QY 61 LRYHLQONVQFSEDVRLYICEMALADYLRGQHIIHRDVKPDNILLDRGHAHLTDENI 120
DB 87 LRYHLQONVQFSEDVRLYICEMALADYLRGQHIIHRDVKPDNILLDRGHAHLTDENI 146
QY 121 ATIIKDGERTALAGTKPYMAPEIFHSPVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 180
DB 147 ATIIKDGERTALAGTKPYMAPEIFHSPVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 206
QY 181 HSSNAVESLVQLFSTVSQVYPTWSKEMV 209
DB 207 HSSNAVESLVQLFSTVSQVYPTWSKEMV 235

RESULT 13
US-10-074-978A-18
; Sequence 18, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
; APPLICANT: Leite, Mario
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Fernandes, Elma
; APPLICANT: Li, Li
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Liu, Xiahong
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Patturajan, Meera
; APPLICANT: Blalock, Angela
; APPLICANT: Ballinger, Robert
; APPLICANT: Vernet, Corine
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Rastelli, Luca

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; APPLICANT: Mezes, Peter S
; APPLICANT: Ellerman, Karen
; APPLICANT: Heyes, Melvin P
; APPLICANT: Heriman, John
; APPLICANT: Pena, Carol E A
; APPLICANT: Shinkete, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Moore, No. US20040010119A11le
; APPLICANT: Shenoy, Suresh
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, Dave
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-269
; CURRENT APPLICATION NUMBER: US/10/074,978A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: 60/268,221
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/335,109
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/312,284
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/268,496
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/276,703
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/330,293
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/322,127
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/280,899
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/310,797
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/268,646
; PRIOR FILING DATE: 2001-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-074-978A-18

Query Match          56.6%; Score 209; DB 4; Length 488;
Best Local Similarity 100.0%; Pred. No. 5.6e-187;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 119 MYAMKMNKQOCIERDEVNVPRELEIQEIEHVFVLNLYWYFQDEDMFMVVDLLGGD 178
QY 61 LRYHLQONVQFSEDVRLYICEMALADYLRGQHIIHRDVKPDNILLDRGHAHLTDENI 120
DB 179 LRYHLQONVQFSEDVRLYICEMALADYLRGQHIIHRDVKPDNILLDRGHAHLTDENI 238
QY 121 ATIIKDGERTALAGTKPYMAPEIFHSPVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 180
DB 239 ATIIKDGERTALAGTKPYMAPEIFHSPVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 298
QY 181 HSSNAVESLVQLFSTVSQVYPTWSKEMV 209
DB 299 HSSNAVESLVQLFSTVSQVYPTWSKEMV 327

RESULT 14
US-10-074-978A-163
; Sequence 163, Application US/10074978A
; Publication No. US20040010119A1

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; GENERAL INFORMATION:
; APPLICANT: Leite, Mario
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Fernandes, Elma
; APPLICANT: Li, Li
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Liu, Xiahong
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Patturajan, Meera
; APPLICANT: Blalock, Angela
; APPLICANT: Ballinger, Robert
; APPLICANT: Vernet, Corine
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter S
; APPLICANT: Ellerman, Karen
; APPLICANT: Heyes, Melvin P
; APPLICANT: Herrman, John
; APPLICANT: Pena, Carol E A
; APPLICANT: Shinkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Moore, No. US20040010119Al11e
; APPLICANT: Shenoy, Suresh
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, Dave
; APPLICANT: Millet, Isabelle
; APPLICANT: Feyman, John
; APPLICANT: Smithson, Glenna
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-269
; CURRENT APPLICATION NUMBER: US/10/074,978A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: 60/268,221
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/335,109
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/312,284
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/268,496
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/276,703
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/330,293
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/322,127
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/280,899
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/310,797
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/268,646
; PRIOR FILING DATE: 2001-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 163
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-10-074-978A-163

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Best Local Similarity 100.0%; Pred. No. 2e-170;
Matches 191; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      25  MYAMKYNKQCCIERDEVNFRFLEILQIEHVFVLNLYWSFQDEEDFMVVDLLLGDD 84

; RESULT 15
US-09-801-876B-6
; Sequence 6, Application US/09801876B
; Patent No. US20020127683A1
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001160
; CURRENT APPLICATION NUMBER: US/09/801,876B
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-801-876B-6

Query Match      30.6%; Score 113; DB 3; Length 384;
Best Local Similarity 100.0%; Pred. No. 4.6e-97;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      171  LLRGWRPYDIHSSNAVESLVOLFSTVSQYVPTWSKEMVALLRKLLTVNPEHR 223
Db      213  LLRGWRPYDIHSSNAVESLVOLFSTVSQYVPTWSKEMVALLRKLLTVNPEHR 265

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Job time : 49 secs

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181  HSSNAVESLVQ 191
205  HSSNAVESLVQ 215
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OM protein - protein search, using sw model

Run on: May 9, 2006, 10:50:58 ; Search time 27 Seconds
(without alignments)
632.558 Million cell updates/sec

Title: US-10-633-631-2

Perfect score: 369

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Searched: 235405 seqs, 46284737 residues

Word size : 1

Total number of hits satisfying chosen parameters: 235171

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA New*

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11: /SIDSS/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
12: /SIDSS/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	300	81.3	375	9 US-10-979-095-12	Sequence 12, Appli
2	35	9.5	225	11 US-11-125-295-5	Sequence 5, Appli
3	35	9.5	236	11 US-11-125-295-7	Sequence 7, Appli
4	35	9.5	364	9 US-10-194-487-572	Sequence 572, App
5	35	9.5	364	9 US-10-195-883-572	Sequence 572, App
6	35	9.5	364	9 US-10-195-888-572	Sequence 572, App
7	35	9.5	364	9 US-10-195-889-572	Sequence 572, App
8	35	9.5	396	11 US-11-125-295-11	Sequence 11, Appl
9	35	9.5	407	11 US-11-125-295-9	Sequence 9, Appli
10	9	2.4	1388	9 US-10-501-035-350	Sequence 350, App
11	8	2.2	256	11 US-11-096-568A-23243	Sequence 23243, A
12	8	2.2	283	9 US-10-506-454-365	Sequence 365, App
13	8	2.2	346	11 US-11-000-365-52	Sequence 52, Appl
14	8	2.2	346	11 US-11-032-794-52	Sequence 52, Appl
15	8	2.2	370	11 US-11-096-568A-23242	Sequence 23242, A
16	8	2.2	377	11 US-11-096-568A-23241	Sequence 23241, A
17	8	2.2	401	11 US-11-000-365-50	Sequence 50, Appl
18	8	2.2	401	11 US-11-032-794-50	Sequence 50, Appl
19	8	2.2	550	11 US-11-113-837-17	Sequence 17, Appl
20	8	2.2	561	11 US-11-090-617-562	Sequence 562, App
21	8	2.2	598	11 US-11-113-837-18	Sequence 18, Appl

22	8	2.2	605	11 US-11-087-099-3240	Sequence 3240, Ap
23	8	2.2	635	11 US-11-113-837-16	Sequence 16, Appl
24	8	2.2	637	11 US-11-113-837-4	Sequence 4, Appli
25	8	2.2	637	11 US-11-087-099-866	Sequence 866, App
26	8	2.2	639	11 US-11-113-837-21	Sequence 21, Appl
27	8	2.2	665	11 US-11-113-837-19	Sequence 19, Appl
28	8	2.2	665	11 US-11-087-099-10870	Sequence 10870, A
29	8	2.2	668	11 US-11-111-239-13	Sequence 13, Appl
30	8	2.2	683	11 US-11-087-099-4971	Sequence 4971, Ap
31	8	2.2	683	11 US-11-087-099-7461	Sequence 7461, Ap
32	8	2.2	683	11 US-11-188-298-17476	Sequence 17476, A
33	8	2.2	1197	9 US-10-055-877-8	Sequence 8, Appli
34	8	2.2	1247	9 US-10-055-877-10	Sequence 10, Appl
35	8	2.2	1372	11 US-11-087-099-3054	Sequence 3054, Ap
36	8	2.2	1372	11 US-11-188-298-13921	Sequence 13921, A
37	8	2.2	1590	9 US-10-055-877-146	Sequence 146, App
38	7	1.9	36	11 US-11-224-106-1	Sequence 1, Appli
39	7	1.9	168	11 US-11-096-568A-11681	Sequence 11681, A
40	7	1.9	169	11 US-11-096-568A-24880	Sequence 24880, A
41	7	1.9	173	11 US-11-096-568A-24879	Sequence 24879, A
42	7	1.9	183	11 US-11-096-568A-14295	Sequence 14295, A
43	7	1.9	193	8 US-10-511-937-2441	Sequence 2441, Ap
44	7	1.9	193	11 US-11-224-106-4	Sequence 4, Appli
45	7	1.9	193	11 US-11-224-106-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

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; Sequence 12, Application US/10979095
; Publication No. US20060068481A1
; GENERAL INFORMATION:
; APPLICANT: INCITE GENOMICS, INC.
; APPLICANT: YANG, Junming
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: BURFORD, Neil
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: REDDY, Roopa
; APPLICANT: YUE, Henry
; APPLICANT: YAO, Monique G.
; APPLICANT: LAL, Preeti
; APPLICANT: KAHN, Farrah A.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: FI-0002 PCT
; CURRENT APPLICATION NUMBER: US/10/979,095
; PRIOR FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/10/168,582
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 60/172,066; 60/176,107; 60/176,107; 60/177,731
; PRIOR FILING DATE: 1999-12-23; 2000-01-14; 2000-01-14; 2000-01-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 12
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 3244919CD1
US-10-979-095-12

Query Match 81.3%; Score 300; DB 9; Length 375;
Best Local Similarity 100.0%; Pred. No. 2.5e+288;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYAMKYNKQOCIERDEVRNFRLETLQIEHVLNLWYSFQDEDMFVVDLLGGD 60

Db 51 MYAMKYNKQOCIERDEVRNFRLETLQIEHVLNLWYSFQDEDMFVVDLLGGD 110

Qy 61 LRYHLQNVQFSEDTVRLYICEMALDYLRGQHIHRDVKPDNILLDERGHAHLTFNI 120

Db 111 LRYHLQONQFSEDTVRLIICENALALDYLRGHIIRHVDKPDNIILLDERGAHLTDFNI 170
QY 121 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 180
Db 171 ATIIKDGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 230
QY 181 HSSNAVESLVOLFSTVSQVPTWSEKEMVALLRKLLTVNPEHRLSSLDQVQAAPALAGVL 240
Db 231 HSSNAVESLVOLFSTVSQVPTWSEKEMVALLRKLLTVNPEHRLSSLDQVQAAPALAGVL 290
QY 241 WDHLSEKRVPEPGVPNKGRLHCDPTFELEBEMILESRLPKKKRLAKNKSRRNDRSSQS 300
Db 291 WDHLSEKRVPEPGVPNKGRLHCDPTFELEBEMILESRLPKKKRLAKNKSRRNDRSSQS 350

RESULT 2

US-11-125-295-5

; Sequence 5, Application US/111125295
; Publication No. US20050287562A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: Novel Human Kinase Proteins and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/11/125,295
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US/10/620,845
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/841,683
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 225
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-125-295-5

Query Match 9.5%; Score 35; DB 11; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.2e-26;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 FLVNLWYSFQDEDMFMVVDLLGGDLRYHLQONV 69
Db 82 FLVNLWYSFQDEDMFMVVDLLGGDLRYHLQONV 116

RESULT 3

US-11-125-295-7
; Sequence 7, Application US/111125295
; Publication No. US20050287562A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: Novel Human Kinase Proteins and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/11/125,295
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US/10/620,845
; PRIOR FILING DATE: 2003-07-15

; PRIOR APPLICATION NUMBER: US/09/841,683
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 236
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-125-295-7

Query Match 9.5%; Score 35; DB 11; Length 236;
Best Local Similarity 100.0%; Pred. No. 1.2e-26;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 FLVNLWYSFQDEDMFMVVDLLGGDLRYHLQONV 69
Db 82 FLVNLWYSFQDEDMFMVVDLLGGDLRYHLQONV 116

RESULT 4

US-10-194-487-572
; Sequence 572, Application US/10194487
; Publication No. US20060074226A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C312
; CURRENT APPLICATION NUMBER: US/10/194,487
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 572
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-194-487-572

Query Match 9.5%; Score 35; DB 9; Length 364;

Best Local Similarity 100.0%; Pred. No. 1.8e-26;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 FLVNLWYSFQDEEDMFVVDLLGGDLRYHLQQNV 69
|||
Db 32 FLVNLWYSFQDEEDMFVVDLLGGDLRYHLQQNV 66

RESULT 5

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US-10-195-883-572
/ Sequence 572, Application US/10195883
/ Publication No. US20060073544A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3430R1C323
/ CURRENT APPLICATION NUMBER: US/10/195,883
/ CURRENT FILING DATE: 2002-07-15
/ Prior Application removed - See File Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 612
/ SEQ. ID. NO 572
/ LENGTH: 364
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-195-883-572

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Query Match      9.5%; Score 35; DB 9; Length 364;
Best Local Similarity 100.0%; Pred. No. 1.8e-26;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 35 FLVNLWYSFQDEDMFWVDLLGGDLRYHLQNV 69
|||
Db 32 FLVNLWYSFQDEDMFWVDLLGGDLRYHLQNV 66

RESULT 6

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US-10-195-888-572
; Sequence 572, Application US/10195888
; Publication No. US20060073545A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C324
; CURRENT APPLICATION NUMBER: US/10/195,888
; CURRENT FILING DATE: 2002-07-15
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 572
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo Sapien

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US-10-195-888-572

Query Match 9.5%; Score 35; DB 9; Length 364;
Best Local Similarity 100.0%; Pred. No. 1.8e-26;
Matches 35; Conservative 0; Mismatches 0; Indels

Qy	35	FLVNLWYSFQDEEDMFVVDLLIIGGDLRYHLQQNV	69
Db <td>32 <th>FLVNLWYSFQDEEDMFVVDLLIIGGDLRYHLQQNV</th> <th>66</th> </td>	32 <th>FLVNLWYSFQDEEDMFVVDLLIIGGDLRYHLQQNV</th> <th>66</th>	FLVNLWYSFQDEEDMFVVDLLIIGGDLRYHLQQNV	66

RESULT 7

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US-10-195-889-572
; Sequence 572, Application US/10195889
; Publication No. US20060074227A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC329
; CURRENT APPLICATION NUMBER: US/10/195,889
; CURRENT FILING DATE: 2002-07-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 572
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-195-889-572

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Query Match          9.5%; Score 35; DB 9; Length 364;
Best Local Similarity 100.0%; Pred. No. 1.8e-26;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 35 FLVNLWYSFQDEEDMFVVDLLIGGDLRYHLQQNV 69
|||

Dp 32 FLVNLWYSFQDEEDMFVVDLLIGGDLRYHLQQNV 66
|||

RESULT 8

```

US-11-125-295-11
; Sequence 11, Application US/11125295
; Publication No. US20050287562A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Doncho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: Novel Human Kinase Proteins and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/11/125,295
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US/10/620,845
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/841,683
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 396
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-125-295-11

Query Match          9.5%; Score 35; DB 11; Length 396;
Best Local Similarity 100.0%; Pred. No. 2e-26;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 FLVNLWYSFQDEDMFMVVDLLGGDLRYHLQNV 69
Db 82 FLVNLWYSFQDEDMFMVVDLLGGDLRYHLQNV 116

RESULT 9
US-11-125-295-9
; Sequence 9, Application US/11125295
; Publication No. US20050287562A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: Novel Human Kinase Proteins and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/11/125,295
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US/10/620,845
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/841,683
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 407
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-125-295-9

Query Match          9.5%; Score 35; DB 11; Length 407;
Best Local Similarity 100.0%; Pred. No. 2e-26;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 FLVNLWYSFQDEDMFMVVDLLGGDLRYHLQNV 69
Db 82 FLVNLWYSFQDEDMFMVVDLLGGDLRYHLQNV 116

RESULT 10
US-10-501-035-350
; Sequence 350, Application US/10501035
; Publication No. US20060046249A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
; TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASE
; FILE REFERENCE: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
; FILE REFERENCE: D0185 PCT
; CURRENT APPLICATION NUMBER: US/10/501,035
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/350,061
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 350
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; LENGTH: 1388
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-035-350

Query Match          2.4%; Score 9; DB 9; Length 1388;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 IHRDVKPDN 104
Db 211 IHRDVKPDN 219

RESULT 11
US-11-096-568A-23243
; Sequence 23243, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23243
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(256)
; OTHER INFORMATION: Ceres Seq. ID no. 12411724
US-11-096-568A-23243

Query Match          2.2%; Score 8; DB 11; Length 256;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 HIIHRDVK 101
Db 46 HIIHRDVK 53

RESULT 12
US-10-506-454-365
; Sequence 365, Application US/10506454
; Publication No. US20060068386A1
; GENERAL INFORMATION:
; APPLICANT: Slesarev, Alexi I
; APPLICANT: Mezhevaya, Katja V
; APPLICANT: Polushin, Nikolai N
; APPLICANT: Shcherbinina, Olga V
; APPLICANT: Shakhova, Vera V
; APPLICANT: Malykh, Andrei G
; APPLICANT: Kozyavkin, Sergei A
; TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophile
; TITLE OF INVENTION: Methanopyrus Kandleri AV19 and Monophyly of Archaeal Methanogens
; FILE REFERENCE: and Methods of Use Thereof
; FILE REFERENCE: FID001
; CURRENT APPLICATION NUMBER: US/10/506,454
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: PCT/US03/06664
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: 60/361,742
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 1722
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 365
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Methanopyrus kandleri
```


US-10-506-454-365

Query Match 2.2%; Score 8; DB 9; Length 283;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 254 VPKNGRLH 261
|||||
Db 6 VPKNGRLH 13

RESULT 13

US-11-000-365-52
; Sequence 52, Application US/11000365
; Publication No. US20050267022A1
; GENERAL INFORMATION:
; APPLICANT: FRANZOSO, GUIDO
; APPLICANT: PAPA, SALVATORE
; APPLICANT: BUBICI, CONCETTA
; APPLICANT: DESMAELE, ENRICO
; APPLICANT: ZAZZERONI, FRANCESCA
; TITLE OF INVENTION: IDENTIFICATION OF NOVEL FACTORS THAT BLOCK PROGRAMMED
; TITLE OF INVENTION: CELL DEATH OR APOPTOSIS BY TARGETING JNK
; FILE REFERENCE: 21459-97705
; CURRENT APPLICATION NUMBER: US/11/000,365
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 60/526,231
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 10/626,905
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 10/263,330
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/328,811
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/326,492
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 52
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Mus musculus

US-11-000-365-52

Query Match 2.2%; Score 8; DB 11; Length 346;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 NILLDERG 111
|||||
Db 175 NILLDERG 182

RESULT 14

US-11-032-794-52
; Sequence 52, Application US/11032794
; Publication No. US20050265970A1
; GENERAL INFORMATION:
; APPLICANT: FRANZOSO, GUIDO
; APPLICANT: PAPA, SALVATORE
; APPLICANT: BUBICI, CONCETTA
; APPLICANT: DESMAELE, ENRICO
; APPLICANT: ZAZZERONI, FRANCESCA
; TITLE OF INVENTION: IDENTIFICATION OF NOVEL FACTORS THAT BLOCK PROGRAMMED
; TITLE OF INVENTION: CELL DEATH OR APOPTOSIS BY TARGETING JNK
; FILE REFERENCE: 21459-97816
; CURRENT APPLICATION NUMBER: US/11/032,794
; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: 11/000,365
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 60/526,231
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: 10/626,905

; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 10/263,330
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/328,811
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/326,492
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 52
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-032-794-52

Query Match 2.2%; Score 8; DB 11; Length 346;
Best Local Similarity 100.0%; Pred. No. 8.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 NILLDERG 111
|||||
Db 175 NILLDERG 182

RESULT 15

US-11-096-568A-23242
; Sequence 23242, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23242
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(370)
; OTHER INFORMATION: Ceres Seq. ID no. 12411723
US-11-096-568A-23242

Query Match 2.2%; Score 8; DB 11; Length 370;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 94 HIIHRDVK 101
|||||
Db 160 HIIHRDVK 167

Search completed: May 9, 2006, 10:55:12
Job time : 28 secs

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 9, 2006, 10:45:32 ; Search time 40 Seconds
(without alignments)
887.600 Million cell updates/sec

Title: US-10-633-631-2
Perfect score: 1942
Sequence: 1 MYAMKYNKQOCIERDEVN.....EAERSALPMCGPICPSAGSG 369

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	754	38.8	379	2 T23688	hypothetical prote
2	458	23.6	733	2 A57459	ribosomal protein
3	453	23.3	380	1 OKBYC2	protein kinase (EC
4	445	22.9	479	2 A38578	protein kinase 2 (
5	445	22.9	752	1 A32571	ribosomal protein
6	444	22.9	740	2 I38556	ribosomal protein
7	439	22.6	733	1 B30001	ribosomal protein
8	434.5	22.4	465	2 S68482	protein kinase ATP
9	432	22.2	648	1 JQ1150	protein kinase (EC
10	429.5	22.1	646	2 T38171	probable serine/th
11	429	22.1	735	2 I51901	ribosomal protein
12	428	22.0	471	2 S68463	protein kinase ATP
13	427	22.0	629	2 A30001	ribosomal protein
14	427	22.0	735	2 A53300	ribosomal protein
15	425.5	21.9	823	2 S48986	probable protein k
16	424	21.8	586	2 A53758	protein kinase C (
17	424	21.8	587	2 A49509	protein kinase C (
18	423	21.8	480	2 S56639	ribosomal protein
19	423	21.8	633	2 C32571	ribosomal protein
20	421.5	21.7	696	2 S55694	protein kinase (EC
21	419	21.6	398	1 OKBYC3	protein kinase (EC
22	417.5	21.5	425	2 S41099	protein kinase (EC
23	416	21.4	351	1 OKWYCB	protein kinase (EC
24	416	21.4	351	1 OKWYCB	protein kinase (EC
25	416	21.4	351	1 OKRTCB	protein kinase (EC
26	416	21.4	480	1 A39360	protein kinase (EC
27	414	21.3	359	2 T21211	hypothetical prote
28	414	21.3	399	1 OKBYC1	protein kinase (EC
29	413	21.3	360	1 OKHUCG	protein kinase (EC

ALIGNMENTS

RESULT 1

T23688

hypothetical protein M03C11.1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T23688

R;McMurray, A.

submitted to the EMBL Data Library, April 1995

A;Reference number: Z19783

A;Accession: T23688

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-379 <WIL>

A;Cross-references: UNIPROT:Q21483; UNIPARC:UPI000007B6C1; EMBL:Z49128; PTDN:CAA88953.1.1

A;Experimental source: clone M03C11

C;Genetics:

A;Gene: CESP:M03C11.1

A;Map position: 3

A;Introns: 41/3; 67/3; 96/3; 127/2; 240/3; 299/2; 358/3

C;Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 38.8%; Score 754; DB 2; Length 379;

Best Local Similarity 43.2%; Pred. No. 1.6e-29;

Matches 140; Conservative 70; Mismatches 106; Indels 8; Gaps 2;

Qy 2 YAMKYNKQOCIERDEVNVRFRLEILQETIEHVFLVNLWYSFQDEDMFVVLDLGGDL 61

Db 54 FALKYNNKRCIEKGAANVIRELTLLSKMHPFIVNLWYTFQDGYMYVSDLLGGDL 113

Qy 62 RYHLQNNVQFSEDTVRLYICEMALADYLRGQHIHRDVKPDNLLDERGHAHLTDENIA 121

Db 114 RYHLSQOGKFAEDRAKYLCEICLAVEYLHEMKIVHRDIKPENILLDEQGHAAHLDNL 173

Qy 122 TIIDKGERATALAGTPYMAPEIFHSFVNGGTGYSEFVDMWSVGVMAYELLRGWRPDIH 181

Db 174 TQLEDQLATSYSGTRPYMAPEIATVLEIEDGVSRSVDWALGVCFYEMLRGTRPEFS 233

Qy 182 SSNAVSLVOLFTSVVQVYPTWSKEMVALLRKLTLVNPHEHLSSLDQVQAAPALAGVLW 241

Db 234 SRTKPEAYVAFRESSTIPYPAHWPTDLIQFINSLMKFDKEKRLVGLBAIKKHSTYERIDF 293

Qy 242 DHLSEKVEPGFVFNKRGHCDPTFELEMLSRPLHKKKRLAKLNKRDNSRDSQSE 301

Db 294 KSVFEKKPSVFIPCKEGLNCNDPMYELERILVSTPIHRRR----TNNHSSGSSSEBPQ 349

Qy 302 NDYLQDCLDIAIQDFVIFNREKLK 325

Db 350 NAALVE----VSAFIDFSRHVK 369

RESULT 2

A57459

F:151-407/Domain: protein kinase homology <KIN>
F:159-167/Region: protein kinase ATP-binding motif

Query Match	22.9%;	Score 445;	DB 2;	Length 479;
Best Local Similarity	33.6%;	Pred. No. 1.1e-14;		
Matches	108;	Conservative 63;	Mismatches 116;	Indels 34; Gaps 9;
Qy	1	MYAMKYNKQOCIERDEVRNVFRELEIQIEHVLVNLWYSFQDEEDMFVVDLLGGD	60	
Db	178	IFAMKVLKDAIARKQVNHKSEKTIQICISHPFIVNLHYAFQTKDKLYVWLVDFVNGGE	237	
Qy	61	LRVHLQNVQSEDTVRLYICEMALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFTNI	120	
Db	238	LFFHLKRGREFSRPRVKIYAAEIVSALDHLHKQDIVYRDLKPENILLDSEGHICITDGL	297	
Qy	121	ATIIKDGGRATAGTKPYMAPEIFHPSFVNGGTGVSFEVDWWSVGMVAYELLRGWRPYDI	180	
Db	298	SKKIETTDGTFTCGTPPEYLAPEVLN-----GHGHCACVDWWSLGLTLLYEMLTGLPFP--	350	
Qy	181	HSSNAVESLVQLFSTVSQV-----VPTW-SKEMVALLRKLTLVNPHEHRLSSL--Q	228	
Db	351	YSQN-----VSTMVQKILNGELKIPTIYISPEAKSLLLEGLLTREVVDKRLGTGKGG	399	
Qy	229	DVQAAPALAGVLWHLSEKRVPGFVNKGRHLHCDPTFELEEMILESRLPHKKKKRLAKN	288	
Db	400	EVKQHPWFKNIDWEKLDKREVEVHFKP-KVKSGTDIS-QIDPVFTQERPMDSLVETSALG	457	
Qy	289	KSRDNRSDSSQSENDYLQCL	309	
Db	458	DAM--GKDTSPGFTYVADSI	476	
RESULT 5				
A32571				
ribosomal protein S6 kinase II (EC 2.7.1.1-) alpha chain homolog - chicken				
C:Species: Gallus gallus (Chicken)				
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004				
C:Accession: A32571				
R:Alcorta, D.A.; Crews, C.M.; Sweet, L.J.; Bankston, L.; Jones, S.W.; Erikson, R.L.				
Mol. Cell. Biol. 9, 3850-3859, 1989				
A:Title: Sequence and expression of chicken and mouse rsk: homologs of Xenopus laevis r1				
A:Reference number: A93113; MUID:89384612; PMID:2779569				
A:Accession: A32571				
A:Molecule type: mRNA				
A:Residues: 1-752 <ALC>				
A:Cross-references: UNIPROT:P18652; UNIPARC:UPI000012DB30; GB:M28488; NID:G551555; PIDN:				
C:Superfamily: ribosomal protein S6 kinase II; protein kinase homology				
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase				
F:78-339/Domain: protein kinase homology <KIN1>				
F:86-94/Region: protein kinase ATP-binding motif				
F:433-692/Domain: protein kinase homology <KIN2>				
Query Match	22.9%;	Score 445;	DB 1;	Length 752;
Best Local Similarity	36.2%;	Pred. No. 1.7e-14;		
Matches	102;	Conservative 51;	Mismatches 113;	Indels 16; Gaps 6;
Qy	1	MYAMKYNKQOCIERDEVRNVFRELEIQIEHVLVNLWYSFQDEEDMFVVDLLGGD	60	
Db	108	LYAMKVLKKAATLKVDRVRVKI-ERDILADVNPFPVKLHYAFQTEGKLYLIDFLRGGD	166	
Qy	61	LRVHLQNVQSEDTVRLYICEMALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFTNI	120	
Db	167	LFTLSKEVMFTEDVKFYLAELALGLDHLHSLGIYIRDLKPENILLDEEGHIKLTDGL	226	
Qy	121	ATIIKDGGE-RATALAGTKPYMAPEIFHPSFVNGGTGVSFEVDWWSVGMVAYELLRGWRPYD	179	
Db	227	SKEAIDHEKKAYSFCGTVEYMAPEVNR-----QCHSHSADWWSYGVLMFEMLTGSLPFG	281	
Qy	180	IHSSNAVESLVQLFSTVSQYVPTWSKEMVALLRKLTLVNPHEHRLSS-----LQDVQAAPA	235	
Db	282	GKORKETMTLILKAKLQMPQFL---SAAQSLRLAFLKFNPNANRLGSGPDGCAEIKRHFP	338	
Qy	236	LAGVLWDLHSEKRVPGFVNKGRHLHCDPTFELEEMILESRLP	277	

Db 339 YSTIDWNKLYRREIKPFPKPAVGQ--PDDTFYFDTEFTSRTP 378

RESULT 6

I38556

Ribosomal protein S6 kinase 2 (EC 2.7.1.1-) 3 - human
N;Alternate names: Insulin-stimulated protein kinase 1 (PK-1, ISPK1); MAP kinase-activat

C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004

C;Accession: I38556; I64835

R;Byrbaek, C.; Vik, R.; Echwald, S.M.; Webb, G.C.; Wang, J.P.; Yang, P.Y.; Vestergaard
Diabetes 44, 90-97, 1995

A;Title: Cloning of a human insulin-stimulated protein kinase (ISPK-1) gene and analysis
nts.

A;Reference number: I38556; MUID:95113220; PMID:7813820

A;Accession: I38556

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-740 <BJO>

A;Cross-references: UNIPROT:P51812; UNIPARC:UPI000012DB2E; EMBL:U08316; NID:G475587; PID

R;Moller, D.E.; Xia, C.H.; Tang, W.; Zhu, A.X.; Jakubowski, M.

Am. J. Physiol. 266, 351-359, 1994

A;Title: Human rsk isoforms: cloning and characterization of tissue-specific expression.

A;Reference number: I51901

A;Accession: I64835

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 2-423, 'L', 425-479, 'N', 481-493, 495-582 <MOJ>

A;Cross-references: UNIPARC:UPI000016AFE6; GB:L07599; GB:L07601; NID:G401773; PIDN:AA8C2

C;Comment: Although ribosomal protein S6 (see PIR:R3HU6) is phosphorylated by this enzym

C;Genetics:

A;Gene: GDB:RPS6KA3; RSK; HU-2; RSK2; HU-3

A;Cross-references: GDB:365648; OMIM:300075

A;Map position: Xp22.2-Xp22.2

C;Superfamily: ribosomal protein S6 kinase II; protein kinase homology

C;Keywords: ATP; monomer; phosphoprotein; phosphotransferase; serine/threonine-specific

F:66-327/Domain: protein kinase homology <KIN1>

F:74-82/Region: protein kinase ATP-binding motif

F:420-679/Domain: protein kinase homology <KIN2>

F:428-436/Region: protein kinase ATP-binding motif

Query Match 22.9%; Score 444; DB 2; Length 740;

Best Local Similarity 36.4%; Pred. No. 1.9e-14;

Matches 100; Conservative 52; Mismatches 105; Indels 18; Gaps 6;

Qy 1 MYAMKYNKQOCIERDEVRNVFRELEIQIEHVLVNLWYSFQDEEDMFVVDLLGGD 60

Db 96 LYAMKVLKKAATLKVDRVRVKM-ERDILVEVNHPPFIVKLYAFQTEGKLYLIDFLRGGD 154

Qy 61 LRVHLQNVQSEDTVRLYICEMALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFTNI 120

Db 155 LFTLSKEVMFTEDVKFYLAELALDHLHSLGIYIRDLKPENILLDEEGHIKLTDGL 214

Qy 121 ATIIKDGGE-RATALAGTKPYMAPEIFHPSFVNGGTGVSFEVDWWSVGMVAYELLRGWRPYD 179

Db 215 SKESIDHEKKAYSFCGTVEYMAPEVNR-----RGHTQSADWWSFGVLMFEMLTGTLFPQ 269

Qy 180 IHSSNAVESLVQLFSTVSQYVPTWSKEMVALLRKLTLVNPHEHRLSS-----LQDVQAAPA 235

Db 270 GKDRKETMTLILKAKLQMPQFL---SAAQSLRLMKFKNPANRLGSGPDGVBSEIKRHSF 326

Qy 236 LAGVLWDLHSEKRVPGFVPNKGR-----LHCDPTF 266

Db 327 FSTIDWNKLYRREIHPPFKPATGRPBDTFFYDPEF 361

RESULT 7

B30001

Ribosomal protein S6 kinase (EC 2.7.1.1-) II alpha chain - African clawed frog
C;Species: Xenopus laevis (African clawed frog)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: B30001

Matches	92;	Conservative	64;	Mismatches	91;	Indels	17;	Gaps	7;
Qy	1	MYAMKYNKQOCIERDEVRNVFRELEIL--QEIHFVLNVLWYSFQDEEDMFVVDLL	57						
Db	436	IYAMKVLSSKVIVKQNEIAHTIGERNILVTTASKSSPFIVGLKFSFQTPTDLYLVTDYMS	495						
Qy	58	GGDLRYHLQONVQPSDTRVLYICEMALADYLRGQHIIHRDVKPDNILLDERGHAHITD	117						
Db	496	GGELFWHLQKEGRFSEDRAKFYIAELVLALSHLHDNDIVYRDLKPENILLDANGNIALCD	555						
Qy	118	FNIAITI-IKQGERATALAGTKPYMAPEIFHSFVNGGTGYSPEVDWWSVGVMAYELLRGWR	176						
Db	556	FGLSKADLKD--RTNTFCGTTEYLAPEL----LLDETGYTKMVDPFWSLGVLIPEMCCGWS	609						
Qy	177	PYDIHSSNAVESLVQLFSTVSVQYV-PTWSKEMVALLRKLLTVNPEHRLSSLQD---VQA	232						
Db	610	PFFAENN--QKMYQKIAFGVKVFPDRDVLSQLGRSFVKGLLNRPKHRLGAIDDGRELRA	666						
Qy	233	APALAGVLWDHLSKRVKVPFGFVN	256						
Db	667	HPFFADIDWEALKQKIPPPKPH	690						

Search completed: May 9, 2006, 10:49:13
Job time : 42 secs

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Db	181	HSSNAVESLVLQSTVSQVPTWSEKVALRLKLTVPNPEHRLSSLDVQAAPALAGVL	240		
Qy	241	WDHLSEKRVPGFVPNKGRLHCDPTFELEEMILESRLPKKKRLAKNKSNDSSQS	300		
Db	241	WDHLSEKRVPGFVPNKGRLHCDPTFELEEMILESRLPKKKRLAKNKSNDSSQS	300		
Qy	301	ENDYLODCLDAIQODFVFNREKLKRSQDLPREPLPAPESRDAEPVEDEAERSALPMCG	360		
Db	301	ENDYLODCLDAIQODFVFNREKLKRSQDLPREPLPAPESRDAEPVEDEAERSALPMCG	360		
Qy	361	PICPSAGSG 369			
Db	361	PICPSAGSG 369			
RESULT 2					
Q86UX6 HUMAN					
ID	Q86UX6	HUMAN PRELIMINARY;	PRT; 486 AA.		
AC	Q86UX6				
DT	01-JUN-2003	(TrEMBLrel. 24, Created)			
DT	01-JUN-2003	(TrEMBLrel. 24, Last sequence update)			
DT	13-SEP-2005	(TrEMBLrel. 31, Last annotation update)			
DE	PKE protein kinase.				
GN	Name=STK32C; Synonyms=RP11-140A10.1; ORFNames=RP11-140A10.1-002;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;				
OC	Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RA	Ma A.-H., Nelson D.A., Xia L., Ravi L., Chen H.-C., Robinson D.R.,				
RA	Kung H.-J.;				
RL	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.				
RN	[2]				
RP	NUCLEOTIDE SEQUENCE.				
RA	Tracey A.;				
RL	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.				
RN	[3]				
RP	NUCLEOTIDE SEQUENCE.				
RA	Brown J.;				
RL	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.				
CC	-1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.				
CC	-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.				
DR	EMBL;	AY098866;	AAW21719.1; -; mRNA.		
DR	EMBL;	AL512622;	CA112181.1; -; Genomic DNA.		
DR	EMBL;	AL590105;	CA113011.1; -; Genomic DNA.		
DR	EMBL;	AL590105;	CA112181.1; JOINED; Genomic DNA.		
DR	EMBL;	AL512622;	CA113011.1; JOINED; Genomic DNA.		
DR	HSSP;	P31751;	1MRV.		
DR	Ensembl;	ENSG00000165752; Homo sapiens.			
DR	HGNC;	HGNC:21332; STK32C.			
DR	GO;	GO:0005524; F:ATP binding; IEA.			
DR	GO;	GO:0004674; P:protein serine/threonine kinase activity; IEA.			
DR	GO;	GO:0006468; P:protein amino acid phosphorylation; IEA.			
DR	InterPro;	IPR000719; Prot kinase.			
DR	InterPro;	IPR008271; Ser_Thr_pkin AS.			
DR	InterPro;	IPR002290; Ser_thr_pkinase.			
DR	Pfam;	PF00069; Pkinase; 1.			
DR	ProDom;	PD000001; Prot_kinase; 1.			
DR	SMART;	SM00220; S_TKC; 1.			
DR	PROSITE;	PS00107; PROTEIN_KINASE_ATP; 1.			
DR	PROSITE;	PS00111; PROTEIN_KINASE_DOM; 1.			
DR	PROSITE;	PS00108; PROTEIN_KINASE_ST; 1.			
KW	ATP-binding; Kinase; Nucleotide-binding;				
KW	Serine/threonine-protein kinase; Transferase.				
SQ	SEQUENCE 486 AA; 54994 MW; 38FEFBB3863B21F3 CRC64;				
Query Match 100.0%; Score 1942; DB 2; Length 486;					
Best Local Similarity 100.0%; Pred. No. 5.3e-120;					
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					

Qy	1	MYAMKMNKQOCIERDEVRNVPRELILQIEHVLVNLWYSFQDEDMFVVDLLGGD	60		
Db	118	MYAMKMNKQOCIERDEVRNVPRELILQIEHVLVNLWYSFQDEDMFVVDLLGGD	177		
Qy	61	LYHLQONQVFSQSDTVRLYICEMALDYLRLGQHIHRDVKPDNILLDERGHAHLTDFTNI	120		
Db	178	LYHLQONQVFSQSDTVRLYICEMALDYLRLGQHIHRDVKPDNILLDERGHAHLTDFTNI	237		
Qy	121	ATIIKDGCRATAGKTPWAPBEIPIHSGFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI	180		
Db	238	ATIIKDGCRATAGKTPWAPBEIPIHSGFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI	297		
Qy	181	HSSNAVESLVLQSTVSQVPTWSEKVALRLKLTVPNPEHRLSSLDVQAAPALAGVL	240		
Db	298	HSSNAVESLVLQSTVSQVPTWSEKVALRLKLTVPNPEHRLSSLDVQAAPALAGVL	357		
Qy	241	WDHLSEKRVPGFVPNKGRLHCDPTFELEEMILESRLPKKKRLAKNKSNDSSQS	300		
Db	358	WDHLSEKRVPGFVPNKGRLHCDPTFELEEMILESRLPKKKRLAKNKSNDSSQS	417		
Qy	301	ENDYLODCLDAIQODFVFNREKLKRSQDLPREPLPAPESRDAEPVEDEAERSALPMCG	360		
Db	418	ENDYLODCLDAIQODFVFNREKLKRSQDLPREPLPAPESRDAEPVEDEAERSALPMCG	477		
Qy	361	PICPSAGSG 369			
Db	478	PICPSAGSG 486			
RESULT 3					
Q86UE1 HUMAN					
ID	Q86UE1	HUMAN PRELIMINARY;	PRT; 369 AA.		
AC	Q86UE1				
DT	01-JUN-2003	(TrEMBLrel. 24, Created)			
DT	01-JUN-2003	(TrEMBLrel. 24, Last sequence update)			
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)			
DE	STK32C protein.				
GN	Name=STK32C;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;				
OC	Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	TISSUE=Testis;				
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,				
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,				
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,				
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;				
RT	"Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences."				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
RN	[2]				
RP	NUCLEOTIDE SEQUENCE.				
RC	TISSUE=Testis;				
RG	NIH MGC Project;				
RL	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.				
DR	EMBL;	BC045760;	AAH45760.1; -; mRNA.		

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DR HSP, P31751; lMRV.
DR Ensembl; ENSG00000165752; Homo sapiens.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR00719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Hypothetical protein; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 369 AA; 42395 MW; E152C66B2D786B4 CRC64;

Query Match 99.7%; Score 1937; DB 2; Length 369;
Best Local Similarity 99.7%; Pred. No. 8.2e-120;
Matches 368; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MYAMKYNKQOCIERDEVRNVFRELEILQIEIHVFLVNLWYSFQDEEDMFVVDLLGGD 60
Db 1 MYAMKYNKQOCIERDEVRNVFRELEILQIEIHVFLVNLWYSFQDEEDMFVVDLLGGD 60

Qy 61 LRYHLQNVQPSDVTVRLYICEMALDYLRGQHIHRDVKPDNILLDERGHAHLTDFTNI 120
Db 61 LRYHLQNVQPSDVTVRLYICEMALDYLRGQHIHRDVKPDNILLDERGHAHLTDFTNI 120

Qy 121 ATTIKQGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVNAYELLGRWPYDI 180
Db 121 ATTIKQGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVNAYELLGRWPYDI 180

Qy 181 HSSNAVESLVQLFSTVSQVYPTWSKEMVALLRKLTVNPEHRLSSLDQVQAAAPALAGVL 240
Db 181 HSSNAVESLVQLFSTVSQVYPTWSKEMVALLRKLTVNPEHRLSSLDQVQAAAPALAGVL 240

Qy 241 WDHLSEKRVPGFVFNKGRHLCDPTFELEEMILESRLPKKKRKLAKNKRSDNRSSQS 300
Db 241 WDHLSEKRVPGFVFNKGRHLCDPTFELEEMILESRLPKKKRKLAKNKRSDNRSSQS 300

Qy 301 ENDYLDQCLDAIQDQFVFNREKLKRSQDLPREPLPAPESRDAEPVEDEAERSALPMCG 360
Db 301 ENDYLDQCLDAIQDQFVFNREKLKRSQDLPREPLPAPESRDAEPVEDEAERSALPMCG 360

Qy 361 PICPSAGSG 369
Db 361 PICPSAGSG 369

RESULT 4
ID Q9BGT4_MACFA PRELIMINARY; PRT; 368 AA.
AC Q9BGT4
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheidae; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Frontal lobe left;
RA Hashimoto K., Oada N., Hida M., Kusuda J., Sugano S.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB056389.1-BAB33045.1; -; mRNA.
DR HSP; P31751; lMRV.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR00719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.

DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Hypothetical protein; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 368 AA; 42218 MW; 5D7269B32DABCC14 CRC64;

Query Match 96.5%; Score 1873.5; DB 2; Length 368;
Best Local Similarity 97.0%; Pred. No. 1.3e-115;
Matches 358; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

Qy 1 MYAMKYNKQOCIERDEVRNVFRELEILQIEIHVFLVNLWYSFQDEEDMFVVDLLGGD 60
Db 1 MYAMKYNKQOCIERDEVRNVFRELEILQIEIHVFLVNLWYSFQDEEDMFVVDLLGGD 60

Qy 61 LRYHLQNVQPSDVTVRLYICEMALDYLRGQHIHRDVKPDNILLDERGHAHLTDFTNI 120
Db 61 LRYHLQNVQPSDVTVRLYICEMALDYLRGQHIHRDVKPDNILLDERGHAHLTDFTNI 120

Qy 121 ATTIKQGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVNAYELLGRWPYDI 180
Db 121 ATTIKQGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVNAYELLGRWPYDI 180

Qy 181 HSSNAVESLVQLFSTVSQVYPTWSKEMVALLRKLTVNPEHRLSSLDQVQAAAPALAGVL 240
Db 181 HSSNAVESLVQLFSTVSQVYPTWSKEMVALLRKLTVNPEHRLSSLDQVQAAAPALAGVL 240

Qy 241 WDHLSEKRVPGFVFNKGRHLCDPTFELEEMILESRLPKKKRKLAKNKRSDNRSSQS 300
Db 241 WDHLSEKRVPGFVFNKGRHLCDPTFELEEMILESRLPKKKRKLAKNKRSDNRSSQS 300

Qy 301 ENDYLDQCLDAIQDQFVFNREKLKRSQDLPREPLPAPESRDAEPVEDEAERSALPMCG 360
Db 301 ENDYLDQCLDAIQDQFVFNREKLKRSQDLPREPLPAPESRDAEPVEDEAERSALPMCG 360

Qy 361 PICPSAGSG 369
Db 361 PICPSAGSG 368

RESULT 5
ID Q8QZV4_MOUSE PRELIMINARY; PRT; 488 AA.
AC Q8QZV4
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Serine/threonine kinase 32C (Mus musculus adult male corpora
DE quadrigena cDNA, RIKEN full-length enriched library,
DE clone:B230385A21 product: hypothetical serine/threonine protein kinase,
DE full insert sequence).
GN Name=Stk32c;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale L.J., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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Qy 61 LRVHLQNVQFSEDTVRLYICEMALADYLRLGQHIHRDVKPNILDERGHAHLTDFNI 120
Db 179 LRVHLQNVQFSEDTVRLYICEMALADYLRLGQHIHRDVKPNILDERGHAHLTDFNI 238
Qy 121 ATTIKGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGMAYELLRGWRPYDI 180
Db 239 ATTIKGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGMAYELLRGWRPYDI 298
Qy 181 HSSNAVESLVQLFSTVSQVPTWSEKEMVALLRKLTVNPEHRLSSLDQVQAAPALAGVL 240
Db 299 HSSNAVESLVQLFSTVSQVPTWSEKEMVALLRKLTVNPEHRLSSLDQVQAAPALAGVL 358
Qy 241 WDHLSEKRVPGFVFNKGRHLCDPTFELEEMILESRLHKKKRLAKNKSRRDSSQS 300
Db 359 WDDLSEKRVPGFVFNKGRHLCDPTFELEEMILESRLHKKKRLAKNKSRRDSSQS 418
Qy 301 ENDYLQCLDAIQODFVIFNREKLKRSQDLPREPLPAPESRDAAPVED-EAERSALPMC 359
Db 419 ENDYLQCLDAIQODFVIFNREKLKRSQELMSEPPPGPETSMDTSTADSEAEPTALPMC 478
Qy 360 GPICPSAGS 368
Db 479 GSICPSSGS 487

RESULT 6
Q9JG4_MOUSE PRELIMINARY; PRT; 488 AA.
ID Q9JG4_MOUSE PRELIMINARY; PRT; 488 AA.
AC Q9JG4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus brain cDNA, clone MNCb-1563, similar to A2750840
DE serine/threonine protein kinase (Mus musculus).
GN Name=Stk32c; Synonyms=Pek;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL;
RA Osada N., Kusuda J., Tanuma R., Ito A., Hirata M., Sugano S.,
RA Hashimoto K.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AB041542; BAA95027.1; -; mRNA.
DR HSP; P31751; INRV.
DR Ensembl; ENSMUSG0000015981; Mus musculus.
DR MGI; MGI:2385336; Stk32c.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR00719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 488 AA; 55277 MW; 310483FF69E24E39 CRC64;
```

Query Match 92.0%; Score 1786.5; DB 2; Length 488;
Best Local Similarity 92.4%; Pred. No. 9.9e-110;
Matches 341; Conservative 10; Mismatches 17; Indels 1; Gaps 1;

Qy 1 MYAMKYNKQOCIERDEVNRFREILQIEHVFVLNLYWYSFQDEEDMFVVDLLGGD 60

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Db 119 MYAMKYNKQOCIERDEVNRFREILQIEHVFVLNLYWYSFQDEEDMFVVDLLGGD 178
Qy 61 LRVHLQNVQFSEDTVRLYICEMALADYLRLGQHIHRDVKPNILDERGHAHLTDFNI 120
Db 179 LRVHLQNVQFSEDTVRLYICEMALADYLRLGQHIHRDVKPNILDERGHAHLTDFNI 238
Qy 121 ATTIKGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGMAYELLRGWRPYDI 180
Db 239 ATTIKGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGMAYELLRGWRPYDI 298
Qy 181 HSSNAVESLVQLFSTVSQVPTWSEKEMVALLRKLTVNPEHRLSSLDQVQAAPALAGVL 240
Db 299 HSSNAVESLVQLFSTVSQVPTWSEKEMVALLRKLTVNPEHRLSSLDQVQAAPALAGVL 358
Qy 241 WDHLSEKRVPGFVFNKGRHLCDPTFELEEMILESRLHKKKRLAKNKSRRDSSQS 300
Db 359 WDDLSEKRVPGFVFNKGRHLCDPTFELEEMILESRLHKKKRLAKNKSRRDSSQS 418
Qy 301 ENDYLQCLDAIQODFVIFNREKLKRSQDLPREPLPAPESRDAAPVED-EAERSALPMC 359
Db 419 ENDYLQCLDAIQODFVIFNREKLKRSQELMSEPPPGPETSMDTSTADSEAEPTALPMC 478
Qy 360 GPICPSAGS 368
Db 479 GSICPSSGS 487

RESULT 7
Q5T0Q4_HUMAN PRELIMINARY; PRT; 381 AA.
ID Q5T0Q4_HUMAN PRELIMINARY; PRT; 381 AA.
AC Q5T0Q4;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Protein kinase (PKE).
GN Name=RP11-140A10.1; ORFNames=RP11-140A10.1-004;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tracey A.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AL512622; CA112188.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TyrKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 381 AA; 43102 MW; 6564FFB4CDF5E333 CRC64;
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Query Match 81.2%; Score 1576; DB 2; Length 381;
Best Local Similarity 100.0%; Pred. No. 5.8e-96;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYAMKYNKQOCIERDEVNRFREILQIEHVFVLNLYWYSFQDEEDMFVVDLLGGD 60

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Db 57 MYAMKYNKQOCLERDEVRNVPFELEILQIEHVFVNLWYSFQDEDMFVWVDLLIGD 116
QY 61 LRYHLQONVQFSDTVRLVYICEMALADYLRGQHHIHRDVKPDNIILLDERGHAHLTDFNI 120
Db 117 LRYHLQONVQFSDTVRLVYICEMALADYLRGQHHIHRDVKPDNIILLDERGHAHLTDFNI 176
QY 121 ATTIKGERATAGTKPYNAPEIFHSFVNGGTGYSFEVDWWSVGVMAVELLRGWRPYDI 180
Db 177 ATTIKGERATAGTKPYNAPEIFHSFVNGGTGYSFEVDWWSVGVMAVELLRGWRPYDI 236
QY 181 HSSNAVESLVOLFSTVSQVYPTWSEKEMVALLRKLTVNPEHRLSSLDQVQAAAPALAGVL 240
Db 237 HSSNAVESLVOLFSTVSQVYPTWSEKEMVALLRKLTVNPEHRLSSLDQVQAAAPALAGVL 296
QY 241 WDHLSEKRVPGFVFNKGRHLHCDPTFELEEMILESRLPHKKKKRLAKNKSNDNSRDSSQS 300
Db 297 WDHLSEKRVPGFVFNKGRHLHCDPTFELEEMILESRLPHKKKKRLAKNKSNDNSRDSSQS 356

RESULT 8
Q4RN62_TETNG
ID Q4RN62 TETNG PRELIMINARY; PRT; 441 AA.
AC Q4RN62;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Chromosome undetermined SCAFI5016, whole genome shotgun sequence.
GN ORFNames=GSTENG0031718001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OC NCBI_TaxID=99883;
RN [1];
RP NUCLEOTIDE SEQUENCE..
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segreus B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anhouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RL the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2];
RP NUCLEOTIDE SEQUENCE.
RA Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: CAAE01015016; CAG10170.1; -; Genomic DNA.
SQ SEQUENCE 441 AA; 50816 MW; 71C91AC5A8E49B63 CRC64;

Query Match 74.8%; Score 1453.5; DB 2; Length 441;
Best Local Similarity 72.9%; Pred. No. 8.5e-88;
Matches 275; Conservative 27; Mismatches 20; Indels 55; Gaps 2;

QY 1 MYAMKYNKQOCLERDEVRNVPFELEILQIEHVFVNLWYSFQDEDMFVWVDLLIGD 60
Db 66 MYAMKYNKQOCLERDEVRNVPFELEILQIEHVFVNLWYSFQDEDMFVWVDLLIGD 125
QY 61 LRYHLQONVQFSDTVRLVYICEMALADYLRGQHHIHRDVKPDNIILLDERGHAHLTDFNI 180
Db 126 LRYHLQONVQFSDTVRLVYICEMALADYLRGQHHIHRDVKPDNIILLDERGHAHLTDFNI 195

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QY 98 -----RDVKPDNIILLDERGHAHLTDFNIATIKD 126
Db 186 LPPYDIFSFKYQWAPGGKLAALNGPACSVTDVDPDNILLDERGHAHLTDFNIATIKD 245
QY 127 GERATAGTKPYNAPEIFHSFVNGGTGYSFEVDWWSVGVMAVELLRGWRPYDIHSSNAV 186
Db 246 GERATAGTKPYNAPEIFHSFVNGGTGYAFVVDWWSVGVMAVELLRGWRPYDIHASNVS 305
QY 187 ESLVOLFTSVSYQVYPTWSEKEMVALLRKLTVNPEHRLSSLDQVQAAAPALAGVLDHLS 246
Db 306 ESLIQLFSTISVOYSPAWPKDLVSLRKLTVNPEHRSLSLDMQTSPLYADIINWDVAYE 365
QY 247 KRVEGFGVFNKGRHLHCDPTFELEEMILESRLPHKKKKRLAKNKSNDNSRDSSQS 306
Db 366 KMEAGFVFNKGRHLHCDPTFELEEMILESRLPHKKKKRLAKNKSNDNSKD-SQSENDY 424
QY 307 DCLDAIQDQDFVFNREK 323
Db 425 ECLDVVQDEFMFNRER 441

RESULT 9
Q8IY14_HUMAN
ID Q8IY14_HUMAN PRELIMINARY; PRT; 414 AA.
AC Q8IY14;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Serine/threonine kinase 32B.
GN Name=STK32B;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2];
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL: BC038236; AAH38236.1; -; mRNA.
DR HSSP: P31751; 1MRV.
DR Ensembl: ENSG00000152953; Homo sapiens.
DR HGNC: HGNC:14217; STK32B.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.

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DR GO: 0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF002290; Ser_thr_pkinase.
DR InterPro; IPR00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 414 AA; 47784 MW; F0E5EE695FA8242F CRC64;

Query Match 65.6%; Score 1273.5; DB 2; Length 414;
Best Local Similarity 69.8%; Pred. No. 6.1e-76;
Matches 229; Conservative 50; Mismatches 48; Indels 1; Gaps 1;

QY 1 MYAMKYNKQOCIERDVRNVFRELEILOEIEHVLVNLWYSFQDEEDMFVVDLLGGD 60
DB 48 MYAMKYNKQOCIERDVRNVFRELEILOEIEHVLVNLWYSFQDEEDMFVVDLLGGD 107
QY 61 LRVHLQONVQFSDTVPLVICEMALDYLRGQHIHRDVKPDNILLDERGHAHLTDFTNI 120
DB 108 LRVHLQONVHFTGTVKLYICELALEYLQRYHIIHRDKPDNILLDEGHVHTDFTNI 167
QY 121 ATTIKGERATAGTKPYMAPEIFHSFVNGTGYSPVDWWSGVWYELLRGWRPYDI 180
DB 168 ATTVKGAERASSMAGTKPYMAPEVQVYMDGGPGYSPVDWWSLGTAYELLRGWRPYEI 227
QY 181 HSSNAVESVLQFSTVSQVYPTWSKEMVALLRKLTVNPEHRLSSLODVOAAPALAGVL 240
DB 228 HSVTPIDEILNMFKVERVHSYSTWCKGMVALLRKLTKDPESRVSSLHDIQSPYVLADMN 287
QY 241 WDHLSEKRVPGFVPVNGRLHCDPTFELEEMILESRLPKKKRKLAKNKRSDNRSSQS 300
DB 288 WDAVFKKALMPGFPVNGRLNCDPTFELEEMILESRLPKKKRKLAKNKRSDGTGKDCPL 347
QY 301 ENDYLODCLDAIQODVFVFNREKLKRSQ 328
DB 348 -NGHLQHCLETVEEFIFNREKLRRQ 374

RESULT 10
Q9NY57 HUMAN PRELIMINARY; PRT; 414 AA.
AC Q9NY57;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Serine/threonine protein kinase.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole brain cDNA;
RX MEDLINE=20164328; PubMed=10700184; DOI=10.1038/73508;
RA Ruiz-Perez V.L., Ide S.E., Strom T.M., Lorenz B., Willson D., Woods K.,
RA King L., Francomano C., Freisinger P., Spranger S., Marino B.,
RA Dallapiccola B., Wright M., Meitinger T., Polymeropoulos M.H.,
RA Goodship J.;
RT "Mutations in a new gene in Ellis-van Creveld syndrome and Weyers
RT acrocardial dysostosis";
RL Nat. Genet. 24:283-286(2000).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR ENBL; AJ250839; CAB76471.1; -; mRNA.
DR HSP; P31751; IMRV.
DR GO: 0005524; F:ATP binding; IEA.
DR GO: 0004674; F:protein serine/threonine kinase activity; IEA.
DR GO: 0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 414 AA; 47883 MW; 8FCD58A67EF09B0E CRC64;

Query Match 65.2%; Score 1265.5; DB 2; Length 414;
Best Local Similarity 69.5%; Pred. No. 2e-75;
Matches 228; Conservative 50; Mismatches 49; Indels 1; Gaps 1;

QY 1 MYAMKYNKQOCIERDVRNVFRELEILOEIEHVLVNLWYSFQDEEDMFVVDLLGGD 60
DB 48 MYAMKYNKQOCIERDVRNVFRELEILOEIEHVLVNLWYSFQDEEDMFVVDLLGGD 107
QY 61 LRVHLQONVQFSDTVPLVICEMALDYLRGQHIHRDVKPDNILLDERGHAHLTDFTNI 120
DB 108 LRVHLQONVHFTGTVKLYICELALEYLQRYHIIHRDKPDNILLDEGHVHTDFTNI 167
QY 121 ATTIKGERATAGTKPYMAPEIFHSFVNGTGYSPVDWWSGVWYELLRGWRPYDI 180
DB 168 ATTVKGAERASSMAGTKPYMAPEVQVYMDRGFGYSPVDWWSLGTAYELLRGWRPYEI 227
QY 181 HSSNAVESVLQFSTVSQVYPTWSKEMVALLRKLTVNPEHRLSSLODVOAAPALAGVL 240
DB 228 HSVTPIDEILNMFKVERVHSYSTWCKGMVALLRKLTKDPESRVSSLHDIQSPYVLADMN 287
QY 241 WDHLSEKRVPGFVPVNGRLHCDPTFELEEMILESRLPKKKRKLAKNKRSDNRSSQS 300
DB 288 WDAVFKKALMPGFPVNGRLNCDPTFELEEMILESRLPKKKRKLAKNKRSDGTGKDCPL 347
QY 301 ENDYLODCLDAIQODVFVFNREKLKRSQ 328
DB 348 -NGHLQHCLETVEEFIFNREKLRRQ 374

RESULT 11
Q7TMD3 MOUSE PRELIMINARY; PRT; 414 AA.
AC Q7TMD3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Serine/threonine kinase 32B.
GN Name=Stk32b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain, and Mouse;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnierch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Mouse;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Mouse;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC052404; AAH52404.1; -; mRNA.
DR EMBL; BC058412; AAH58412.1; -; mRNA.
DR EMBL; BC056396; AAH56396.1; -; mRNA.
DR HSSP; P31751; IMRV.
DR Ensembl; ENSMUSG00000015981; Mus musculus.
DR MGI; MGI:1927552; Stk32b.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 414 AA; 47916 MW; 3C394415790594F3 CRC64;

Query Match 64.9%; Score 1260.5; DB 2; Length 414;
Best Local Similarity 68.9%; Pred. No. 4.4e-75;
Matches 226; Conservative 55; Mismatches 46; Indels 1; Gaps 1;

QY 1 MYAMKYNKQOCIERDEVRNVFREILQIEHVFVLNLYWYFQDEDMFMVVDLLGGD 60
DB 48 MYAMKYNKQKQKVERDEVRNVFREILQMQGLEHPLVNLWYFQDEDMFMVVDLLGGD 107

QY 61 LRYHLQONVQFSDTVRLVICEMALDYLRCQHIIHRDVKPDNILLDRGHAHLTDFNI 120
DB 108 LRYHLQONVHFTEGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDRGHVHIITDFNI 167

QY 121 ATIIKDGERTALAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 180
DB 168 ATVLKGSEKASSMAGTKPYMAPEVQVYVDGGGYSYPVDMWSLGVATYELLRGWRPYEI 227

QY 181 HSSNAVESLVQLPSTVSQVVPVTSKEMVALLRKLITVNPPEHRLSLQDVQAAPALAGVL 240
DB 228 HSATPIDEILNMFKVERVHYSTWCCEGMSLLKLLTKDPESRLSLRDIQSTYLDNWN 287

QY 241 WDHLSEKRVPEGVFNKGRHLCDPTFELBEMILESRLPHKKKRLAKNKRSDNRSSQS 300
DB 288 WDAVFEKALMPGVFNKGRNLCDPTFELBEMILESRLPHKKKRLAKNKRSDNRSSQS 347

QY 301 ENDYLQDCLDAIQDQDFVFNREKLKRSQ 328
DB 348 -NGHLOQCLETVRKEFIIFNREKLRRQQ 374

RESULT 12
Q9JUX8_MOUSE
ID Q9JUX8_MOUSE PRELIMINARY; PRT; 414 AA.

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AC O9JUX8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Serine/threonine protein kinase.
GN Name=Stk32b; Synonyms=Stk32;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain CDNA;
RX MEDLINE=20164328; PubMed=10700184; DOI=10.1038/73508;
RA Ruiz-Perez V.L., Ide S.E., Strom T.M., Lorenz B., Wilson D., Woods K.,
RA King L., Francomano C., Freisinger P., Spranger S., Marino B.,
RA Dallapiccola B., Wright M., Meitinger T., Polymeropoulos M.H.,
RA Goodship J.;
RT "Mutations in a new gene in Ellis-van Creveld syndrome and Meyers
RT acrocardial dysostosis.";
RL Nat. Genet. 24:283-286(2000).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AJ250840; CAB76566.1; -; mRNA.
DR HSSP; P31751; IMRV.
DR Ensembl; ENSMUSG00000015981; Mus musculus.
DR MGI; MGI:1927552; Stk32b.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 414 AA; 47917 MW; BE394415790B9A13 CRC64;

Query Match 64.9%; Score 1260.5; DB 2; Length 414;
Best Local Similarity 68.9%; Pred. No. 4.4e-75;
Matches 226; Conservative 55; Mismatches 46; Indels 1; Gaps 1;

QY 1 MYAMKYNKQOCIERDEVRNVFREILQIEHVFVLNLYWYFQDEDMFMVVDLLGGD 60
DB 48 MYAMKYNKQKQKVERDEVRNVFREILQMQGLEHPLVNLWYFQDEDMFMVVDLLGGD 107

QY 61 LRYHLQONVQFSDTVRLVICEMALDYLRCQHIIHRDVKPDNILLDRGHAHLTDFNI 120
DB 108 LRYHLQONVHFTEGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDRGHVHIITDFNI 167

QY 121 ATIIKDGERTALAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 180
DB 168 ATVLKGSEKASSMAGTKPYMAPEVQVYVDGGGYSYPVDMWSLGVATYELLRGWRPYEI 227

QY 181 HSSNAVESLVQLPSTVSQVVPVTSKEMVALLRKLITVNPPEHRLSLQDVQAAPALAGVL 240
DB 228 HSATPIDEILNMFKVERVHYSTWCCEGMSLLKLLTKDPESRLSLRDIQSTYLDNWN 287

QY 241 WDHLSEKRVPEGVFNKGRHLCDPTFELBEMILESRLPHKKKRLAKNKRSDNRSSQS 300
DB 288 WDAVFEKALMPGVFNKGRNLCDPTFELBEMILESRLPHKKKRLAKNKRSDNRSSQS 347

QY 301 ENDYLQDCLDAIQDQDFVFNREKLKRSQ 328
DB 348 -NGHLOQCLETVRKEFIIFNREKLRRQQ 374

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RESULT 13
Q8C4E0 MOUSE
ID Q8C4E0 MOUSE PRELIMINARY; PRT; 414 AA.
AC Q8C4E0;
DT 01-MAR-2003 (TrEMBLrel. 23, last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
DE Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched
DE library, clone:C230053G02 product:serine threonine kinase 32, full
DE insert sequence.
GN Name=Stk32b; Synonyms=Stk32;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikolaio I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Haegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA The FANTOM Consortium;
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuani T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Tanaka S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AK082468; BAC38500.1; -; mRNA.
DR HSSP; P31751; 1MRV.
DR MGI; MGI:1927552; Stk32b.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004668; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00101; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 414 AA; 47884 MW; 9C394364BE19E945 CRC64;
Query Match 64.9%; Score 1259.5; DB 2; Length 414;
Best Local Similarity 68.9%; Pred. No. 5,1e-75;
Matches 226; Conservative 55; Mismatches 46; Indels 1; Gaps 1;
QY 1 MYAMKYNKQOCIERDEVRNFRLEILQIEHVLVNLWYSFQDEDMFVVDLLGGD 60
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
48 MYAMKYNKQKCVDERVNRVRELQIMQGLEHPFLVNLWYSFQDEDMFVVDLLGGD 107
QY 61 LRVHLCQNVQFSDTVRLVTCMALDYLRCQHIIHRDVKPDNILLDERGHAHLDTFNI 120
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
108 LRVHLCQNVHFTGTVKLYICELALEVLRQVHIIHRDKPNILLDEGHVHITDFNI 167
QY 121 ATLIKDGERRATLAGTKPYMAPEIFHSFVNGGTGYSFVDVMSVGMAYELLGRWPYDI 180
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
168 ATVLKSGEKASSVAGTKPYMAPEVQVVDGPGYSVPVDMWSLGVTAVELLGRWPYEI 227
QY 181 HSSNAVESLVOLPSTVSQVPTWSEKMWALLAKLITVNPHEHRLSLQDVQAPALAGVL 240
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
228 HSATPIDTEILNMPKVERVHYSSTWCEGMVSLKLLTKDPESLRLSDIQSTYTLADMN 287
QY 241 WDHLSEKRVEPGPVPKNGKRLHCDPTFELEEMILESRLPKKKKRLAKNKRDRNRSQS 300
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
288 WDAVFKAALMPGVPKNGKRLNCDPTFELEEMILESRLPKKKKRLAKNKRDRNRSQS 347
QY 301 ENDYLDQCLDAIQDQFVFNREKLKRSQ 328
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
348 -NGHLQOCLETVEKFIIFNREKLKRSQ 374
RESULT 14
Q6UXH3_HUMAN
ID Q6UXH3_HUMAN PRELIMINARY; PRT; 364 AA.

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AC O6UXH3;
 DT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DE HSA250839.
 GN ORFNames=UNQ3003;
 GN NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22887236; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.D., Abaya E., Baker K., Baldwin D.T., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshigiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R.L., Watanabe C., Wleand D., Woods K., Xie M.-H.,
 RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
 RA Wood W.I., Godowski P.J., Gray A.M.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 DR EMBL: AY358353; AAQ88719.1; -; mRNA.
 DR HSSP: P05132; 1APM.
 DR Ensembl: ENSG00000152953; Homo sapiens.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO: GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR000719; Prot kinase.
 DR InterPro: IPR008271; Ser Thr pkin AS.
 DR InterPro: IPR022290; Ser Thr kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Prot kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: PS00219; TyrKc; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS01008; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS01008; PROTEIN_KINASE_ST; 1.
 SQ SEQUENCE 364 AA; 42195 MW; FE52D0CB54C7A27C CRC64;
 Query Match 64.3%; Score 1249.5; DB 2; Length 364;
 Best Local Similarity 69.2%; Pred. No. 2e-74;
 Matches 225; Conservative 50; Mismatches 49; Indels 1; Gaps 1;
 QY 4 MKYMNKQCIERDEVRNVPRELEIQLQIEHVFVLNLYWSFQDEDMFMVVDLLGGDLRY 63
 Db 1 MKYMNKQCIERDEVRNVPRELEIQLQIEHVFVLNLYWSFQDEDMFMVVDLLGGDLRY 60
 QY 64 HLOQNVQFSEDTVRLICEMALDYLRCQHIIHRDVKPDNILLDRGHAHLTDENIAT 123
 Db 61 HLOQNVHFTGTVKLYICELALAYLQRYIIHRDVKPDNILLDRGHAHLTDENIATV 120
 QY 124 IKDGERATAGTKPYMAPPEIHFHSFVNGGTGYSFVDSVGMVAYELLRGWRPYDIHSS 183
 Db 121 VKGAERASSWAGTKPYMAPEVFOVYWDGPGVGSYPVDSVLSGLTAYELLRGWRPYEIHVS 180
 QY 184 NAVESLVQLFSTVSQVYPTWSEKVMALLRKLTVNPEHRLSLQDQAPALAGVLWDH 243
 Db 181 TPIDEILNMFKVRVHYSSTWCKGVALRLKLTDPESRVSSLSLHDIQSVPLADNMWDA 240
 QY 244 LSEKRVPGFVPGKRLHCDPTPELEEMILESPLHKKKRLAKNRSNDRSSQSEND 303
 Db 241 VFKKALMPGFPVPGKRLNCDPTPELEEMILESPLHKKKRLAKNRSRDTKDCSPL-NG 299
 QY 304 YLQDCLDAIQDQDFVFNREKLKRSQ 328
 Db 300 HLOQCLTVEEFIIENREKLRRQ 324

RESULT 15
 QBBGW6 MOUSE
 ID QBBGW6 MOUSE PRELIMINARY; PRT; 398 AA.
 AC QBBGW6;
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-FEB-2005 (Tremblrel. 29, Last annotation update)
 DE Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length
 DE enriched library, clone:9630050F05 product:SIMILAR TO SERINE THREONINE
 DE KINASE 32 homolog (Mus musculus 7 days neonate cerebellum cDNA, RIKEN
 DE full-length enriched library, clone:A730009C22 product:SIMILAR TO
 DE SERINE THREONINE KINASE 32 homolog) (Mus musculus adult retina cDNA,
 DE RIKEN full-length enriched library, clone:A930015B13 product:SIMILAR
 DE TO SERINE THREONINE KINASE 32 homolog).
 GN Name=Stk32a;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasekawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guskinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ringwald M., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Oatso N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami Y., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Valeriano R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573 (2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630 (2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Hashiwaagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771 (2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Retina;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR ENBL; AK036266; BAC29366.1; -; mRNA.
 DR ENBL; AK042599; BAC31302.1; -; mRNA.
 DR ENBL; AK044474; BAC31941.1; -; mRNA.
 DR HSSP; P31751; IGZK.
 DR Ensembl; ENSMUSG00000039954; Mus musculus.
 DR MGI; MGI:2442403; Stk32a.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR008271; Ser_thr_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Nucleotide-binding;
 KW Serine/threonine-protein kinase; Transferase.

SQ SEQUENCE 398 AA; 46509 MW; 689BCA5B25CF18BB CRC64;
 Query Match 59.6%; Score 1157; DB 2; Length 398;
 Best Local Similarity 63.0%; Pred. No. 2.8e-68;
 Matches 220; Conservative 51; Mismatches 74; Indels 4; Gaps 2;
 QY 1 MYAMKTMKQOCIERDEVNRFRELEIQLQIEIHVFLVNLWYFQDEEDFMVVDLLGGD 60
 DB 48 MYAMKTMKQKQVERNEVRNFKELQIMQGLEHPLVNLWYFQDEEDFMVVDLLGGD 107
 QY 61 LRYHLQONVQFSEDTVRLVICSMALADYLRGQHIIHROVKPDNILLDERGHAHLTDENI 120
 DB 108 LRYHLQONVHFQEDTVKLFICELAMALDYLSQRIIHRDMKPDNILLDEGHVHTDENI 167
 QY 121 ATIIIDGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWPRYDI 180
 DB 168 AAMLPKEITITVAGTKPYMAPEMTS--RKEGTGYSFAVDWMSLGTAYELLRGPRPYHI 225
 QY 181 HGSNAVESLVQLFSTVSVQVPTWSEKEMVALLRKLITVNPHEHRLSSLDQVQAAPALAGVL 240
 DB 226 RSTSSKEIVNMFETAIVTYPYSAWSQEMVSLKLLKLEPNPDQRFSLHTDIQNFPYMSDMN 285
 QY 241 WDHLSEKRVPEGFVNKGRHLCDPTFELEEMILESRLHKKKKRLAKNKSRRNSRSSQS 300
 DB 286 WDAVLQKRLIPGFIPTKGRINCDDPTFELEEMILESRLHKKKKRLAKREKMKKSSQS 345
 QY 301 ENDYLQDCDLAIQQDFVFNREKLKESQDLPREPLAPESRDAAPVED 349
 DB 346 --CLIQEHLDAVQKGFIFNREKVKSDFNQRQANLALEQTKNTEBED 392
 Search completed: May 9, 2006, 10:47:45
 Job time: 114 secs

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OM protein - protein search, using sw model

Run on: May 9, 2006, 10:42:46 ; Search time 185 Seconds
(without alignments)
876.383 Million cell updates/sec

Title: US-10-633-631-2
Perfect score: 1942
Sequence: 1 MYAMKYNKQCIERVRN.....EAGSALPMGCPICPSAGSG 369

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: genesecp1980s:*
2: genesecp1990s:*
3: genesecp2000s:*
4: genesecp2001s:*
5: genesecp2002s:*
6: genesecp2003as:*
7: genesecp2003bs:*
8: genesecp2004s:*
9: genesecp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1942	100.0	369	5	ABB84299 Human ser
2	1942	100.0	369	7	ADJ70605 Human hea
3	1942	100.0	486	8	ADJ96618 Human YAN
4	1942	100.0	486	8	ADK71861 Human kin
5	1939	99.8	425	4	AAM40592 Human pol
6	1933	99.5	419	4	AAB65599 Novel pro
7	1933	99.5	419	8	ADI29204 Human MAR
8	1927.5	99.3	488	6	ABOI4992 Human NOV
9	1924	99.1	419	4	AAM38806 Human pol
10	1873.5	96.5	368	5	ABB84301 Macaque s
11	1856.5	95.6	713	5	ABB06090 Human NS
12	1845	95.0	364	5	AAOI17708 Human ser
13	1827.5	94.1	485	5	AAE24141 Human kin
14	1786.5	92.0	399	5	ABB84300 Murine se
15	1786.5	92.0	488	5	AAOI17709 Murine se
16	1710	88.1	384	6	ABU62279 Mouse ser
17	1710	88.1	384	8	ADL09166 Mouse ser
18	1710	88.1	384	9	ADZ58502 Mouse ser
19	1693	87.2	444	6	AAE37974 Human kin
20	1576	81.2	375	4	AAE04371 Human kin
21	1576	81.2	442	7	ADG74653 Human kin
22	1340	69.0	429	4	AAB71961 Human TGF
23	1265.5	65.2	403	6	ABU62278 Human ser
24	1265.5	65.2	403	8	ADL09165 Human ser

25	1265.5	65.2	403	9	ADZ58501 Human ser
26	1265.5	65.2	414	4	AAB65600 Novel pro
27	1265.5	65.2	414	5	ABP43807 Serine/th
28	1265.5	65.2	414	5	AAOI17710 Human ser
29	1265.5	65.2	414	6	ABR58617 Human can
30	1265.5	65.2	414	7	ADJ38375 Human pro
31	1265.5	65.2	414	8	ADI29205 Human MAR
32	1265.5	65.2	414	8	ADQ17598 Human sof
33	1260.5	64.9	403	9	ADZ58505 Mouse ser
34	1250	64.4	404	6	ABU62277 Mouse ser
35	1250	64.4	404	8	ADL09164 Mouse ser
36	1250	64.4	404	9	ADZ58500 Mouse ser
37	1249.5	64.3	364	4	AAU29309 Human PRO
38	1249.5	64.3	364	6	ABU58685 Human PRO
39	1249.5	64.3	364	6	ABU88233 Novel hum
40	1249.5	64.3	364	6	ABU84548 Human sec
41	1249.5	64.3	364	6	ABR66422 Human sec
42	1249.5	64.3	364	6	ABR65812 Human sec
43	1249.5	64.3	364	6	ABU99752 Human sec
44	1249.5	64.3	364	6	ABU82991 Human PRO
45	1249.5	64.3	364	6	ABU90112 Novel hum

ALIGNMENTS

RESULT 1	
ABB84299	
ID	ABB84299 standard; protein; 369 AA.
XX	
AC	ABB84299;
XX	
DT	12-NOV-2002 (first entry)
XX	
DE	Human serine/threonine protein kinase subfamily-related protein.
XX	
KW	Serine/threonine protein kinase subfamily; chromosome 10; human; enzyme; cytosolic; gene therapy; drug screening; tissue typing; prostate; lung; pharmacogenomic; brain.
KW	
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Modified-site 42..45
FT	/note= "casein kinase II phosphorylation site"
FT	Modified-site 75..77
FT	/note= "protein kinase C phosphorylation site"
FT	Region 95..107
FT	/note= "serine/threonine protein kinase active signature motif"
FT	Modified-site 152..157
FT	/note= "N-myristoylation site"
FT	Region 185..205
FT	/note= "helix region"
FT	Modified-site 226..229
FT	/note= "casein kinase II phosphorylation site"
FT	Modified-site 245..247
FT	/note= "protein kinase C phosphorylation site"
FT	Modified-site 288..291
FT	/note= "N-glycosylation site"
FT	Modified-site 298..301
FT	/note= "casein kinase II phosphorylation site"
FT	Modified-site 300..303
FT	/note= "casein kinase II phosphorylation site"
XX	WO200259288-A2.
PD	01-AUG-2002.
XX	
PF	15-JAN-2002; 2002WO-US000930.
XX	
PR	23-JAN-2001; 2001US-0263162P.
PR	29-MAR-2001; 2001US-00819607.

XX (PEKE) PE CORP NY.
XX Beasley EM, Ye J, Yan C, Ketchum KA, Di Francesco V;
XX WPI; 2002-599781/64.
XX N-PSDB; ABQ76181, ABQ76182.
XX New peptides related to serine/threonine protein kinase subfamily, useful
PT for treating disorders associated with abnormal expression of kinase in
PT prostate, lungs and brain, in drug screening assays and pharmacogenomic
PT analysis.
XX Claim 1; Fig 2A; 86pp; English.
XX This invention describes a novel serine/threonine protein kinase
CC subfamily-associated protein isolated from human chromosome 10 which has
CC cytostatic activity and can be used for gene therapy. The products of the
CC invention are useful in substantial and specific assays related to
CC functional information of the peptide sequences, to raise antibodies or
CC to elicit immune response, as reagents in assays to determine the levels
CC of protein in biological fluids, and as markers for tissues where the
CC corresponding protein is expressed. The peptides and antibodies are
CC useful in drug screening assays, tissue typing and pharmacogenomic
CC analysis. They are also useful in treating disorders associated with the
CC absence of, inappropriate, or unwanted expression of kinase protein in
CC prostate, lungs or brain. The nucleic acid molecules are useful for
CC probes, primers and chemical intermediates in biological assays, for
CC constructing recombinant vectors, expressing antigenic portions of the
CC protein. The peptide and nucleic acid sequences are useful as models for
CC the development of human therapeutic targets, aid in the identification
CC of therapeutic proteins and serve as targets for the development of human
CC therapeutic agents that modulate kinase activity in cells and tissues
CC that express the kinase. The host cells are useful in producing a kinase
CC protein or peptide, and non-human transgenic animals. This sequence
CC represents the human serine/threonine protein kinase subfamily-associated
CC protein described in the disclosure of the invention
XX Sequence 369 AA;

Query Match 100.0%; Score 1942; DB 5; Length 369;
Best Local Similarity 100.0%; Pred. No. 3.5e-178;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYAMKYNKQOCIERDEVNFRVLEILQIEIHVFLVNLWYSFQDEDMFMVVDLLGGD 60
DB 1 MYAMKYNKQOCIERDEVNFRVLEILQIEIHVFLVNLWYSFQDEDMFMVVDLLGGD 60
QY 61 LRYHLQONVQFSEDVTRLYICEMALDYLRCQHIIHRDVKPDNILLDRGHAHLTDFNI 120
DB 61 LRYHLQONVQFSEDVTRLYICEMALDYLRCQHIIHRDVKPDNILLDRGHAHLTDFNI 120
QY 121 ATIIKDGERTALAGTKPMAPETPHSFVNGGTGYSFEVDWWSVGVMAYELLGRWPYDI 180
DB 121 ATIIKDGERTALAGTKPMAPETPHSFVNGGTGYSFEVDWWSVGVMAYELLGRWPYDI 180
QY 181 HSSNAVESLVQLFSTVSQVYPTWSEKEMVALLRKLITVNPHERLSSLDQVQAPALAGVL 240
DB 181 HSSNAVESLVQLFSTVSQVYPTWSEKEMVALLRKLITVNPHERLSSLDQVQAPALAGVL 240
QY 241 WDHLSEKRVPGFVFNKGLHCDPTFELEEMTLESRLPHKKYKRLAKNKSNDSDSS 300
DB 241 WDHLSEKRVPGFVFNKGLHCDPTFELEEMTLESRLPHKKYKRLAKNKSNDSDSS 300
QY 301 ENDYLQDCLDALQQDFVFNREKLKRSQDLPRELPAPESRDAAEPVEDEASRLPMCG 360
DB 301 ENDYLQDCLDALQQDFVFNREKLKRSQDLPRELPAPESRDAAEPVEDEASRLPMCG 360
QY 361 PICPSAGSG 369
DB 361 PICPSAGSG 369

RESULT 2
ADJ70605
ID ADJ70605 standard; protein; 369 AA.
XX
AC ADJ70605;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human heat mitochondrial protein as a therapeutic target SeqID2411.
XX
DE mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX Homo sapiens.
OS
PN WO2003087768-A2.
XX
PD 23-OCT-2003.
XX
PP 04-APR-2003; 2003WO-US010870.
XX
PR 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-0389987P.
PR 20-SEP-2002; 2002US-0412418P.
XX
XX (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
XX
XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
XX WPI; 2003-845369/78.
XX
XX Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX
PS Claim 1; SEQ ID NO 241; 180pp; English.
XX
XX This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nontropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
SQ Sequence 369 AA;
Query Match 100.0%; Score 1942; DB 7; Length 369;
Best Local Similarity 100.0%; Pred. No. 3.5e-178;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYAMKYNKQOCIERDEVNFRVLEILQIEIHVFLVNLWYSFQDEDMFMVVDLLGGD 60
DB 1 MYAMKYNKQOCIERDEVNFRVLEILQIEIHVFLVNLWYSFQDEDMFMVVDLLGGD 60
QY 61 LRYHLQONVQFSEDVTRLYICEMALDYLRCQHIIHRDVKPDNILLDRGHAHLTDFNI 120

Db 61 LRYHLQONQVQFSEDTVRLYICEMALDYLRGQHHIHRDVKPDNILLDERGHAHLTD FNI 120
QY 121 ATIIKDGGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGMAYELLRGWRPYDI 180
Db 121 ATIIKDGGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGMAYELLRGWRPYDI 180
QY 181 HSSNAVESLVQLFSTVSQVPTWTSKEMVALLRKLTVNPEHRLSSLDQVQAAPALAGVL 240
Db 181 HSSNAVESLVQLFSTVSQVPTWTSKEMVALLRKLTVNPEHRLSSLDQVQAAPALAGVL 240
QY 241 WDHLSEKRVPGFVFNKGRHLCDPTFELEMILESRLPKKKRKLAKNKSNDNRSSQS 300
Db 241 WDHLSEKRVPGFVFNKGRHLCDPTFELEMILESRLPKKKRKLAKNKSNDNRSSQS 300
QY 301 ENDYLDQCLDAIQDDFVFNREKLKRSQDLPREPLPAPESRDAAPVEDEAERSALPMCG 360
Db 301 ENDYLDQCLDAIQDDFVFNREKLKRSQDLPREPLPAPESRDAAPVEDEAERSALPMCG 360
QY 361 PICPSAGSG 369
Db 361 PICPSAGSG 369
RESULT 3
ADJ96618
ID ADJ96618 standard; protein; 486 AA.
AC ADJ96618;
XX
DT 06-MAY-2004 (first entry)
DE Human YANK3 protein SeqID 75.
XX
KW kinase; human; tyrosine protein kinase; serine/threonine protein kinase;
KW PK; STK; gene therapy; cancer; immune-related disease;
KW cardiovascular disease; brain; neuronal associated disease; metabolic;
KW inflammatory disorder; cytostatic; neuroprotective; immunomodulator;
KW antiinflammatory; enzyme; YANK3.
OS Homo sapiens.
OS 28.
XX
XX WO2004006838-A2.
XX
XX 22-JAN-2004.
XX
XX 15-JUL-2003; 2003WO-US021730.
XX
XX 15-JUL-2002; 2002US-0395632P.
XX
XX (SUGE-) SUGEN INC.
XX
XX Whyte D, Manning G, Caenepeel S;
PI WPI; 2004-122753/12.
DR N-PSDB; ADJ96552.
XX
XX New nucleic acid molecule encoding a kinase polypeptide, useful for
PT preparing a composition for treating diseases or disorders, e.g., cancer,
PT or neurological, immunological or inflammatory disorders.
XX
XX Claim 1; SEQ ID NO 75; 366pp; English.
XX
XX This invention relates to a novel isolated, enriched or purified nucleic
XX acid molecule that encodes a kinase polypeptide. Specifically, it relates
XX to human tyrosine and serine/threonine protein kinases (PTK's and STK's),
XX as well as protein kinase-like enzymes. The present invention describes
XX screening methods to identify agonists, antagonists and antibodies that
XX can be used to modulate the activity or function of the mammalian kinase
XX enzymes. As such, these compositions can be used for gene therapy
XX purposes to treat diseases or disorders including cancer, immune-related
XX diseases, cardiovascular disease, brain or neuronal associated disease,
XX metabolic and inflammatory disorders. Accordingly, they exhibit

CC cytosolic, neuroprotective, immunomodulator and antiinflammatory
CC activities. This polypeptide sequence is a human kinase protein sequence
XX of the invention.
SQ Sequence 486 AA;
Query Match 100.0%; Score 1942; DB 8; Length 486;
Best Local Similarity 100.0%; Pred. No. 5.1e-178;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYAMKTMKQOCIERDEVNVPFRELILQIEIHVFLVNLWYSFQDEDMFMVVDLLGGD 60
Db 118 MYAMKTMKQOCIERDEVNVPFRELILQIEIHVFLVNLWYSFQDEDMFMVVDLLGGD 177
QY 61 LRYHLQONQVQFSEDTVRLYICEMALDYLRGQHHIHRDVKPDNILLDERGHAHLTD FNI 120
Db 178 LRYHLQONQVQFSEDTVRLYICEMALDYLRGQHHIHRDVKPDNILLDERGHAHLTD FNI 237
QY 121 ATIIKDGGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGMAYELLRGWRPYDI 180
Db 238 ATIIKDGGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGMAYELLRGWRPYDI 297
QY 181 HSSNAVESLVQLFSTVSQVPTWTSKEMVALLRKLTVNPEHRLSSLDQVQAAPALAGVL 240
Db 298 HSSNAVESLVQLFSTVSQVPTWTSKEMVALLRKLTVNPEHRLSSLDQVQAAPALAGVL 357
QY 241 WDHLSEKRVPGFVFNKGRHLCDPTFELEMILESRLPKKKRKLAKNKSNDNRSSQS 300
Db 358 WDHLSEKRVPGFVFNKGRHLCDPTFELEMILESRLPKKKRKLAKNKSNDNRSSQS 417
QY 301 ENDYLDQCLDAIQDDFVFNREKLKRSQDLPREPLPAPESRDAAPVEDEAERSALPMCG 360
Db 418 ENDYLDQCLDAIQDDFVFNREKLKRSQDLPREPLPAPESRDAAPVEDEAERSALPMCG 477
QY 361 PICPSAGSG 369
Db 478 PICPSAGSG 486
RESULT 4
ADK71861
ID ADK71861 standard; protein; 486 AA.
XX
AC ADK71861;
XX
DT 20-MAY-2004 (first entry)
DE Human kinase and phosphatase KPP-38 protein.
XX
KW human; kinase; phosphatase; KPP; cardiovascular; antiarteriosclerotic;
KW hypotensive; vasotropic; antiinflammatory; antianginal; anti-HIV;
KW antiallergic; antisthmatic; immunosuppressive; antithyroid;
KW dermatological; antidiabetic; nephrotropic; angiot; gastrointestinal;
KW neuroprotective; osteopathic; antiarthritic; uropathic; ophthalmological;
KW antirheumatic; antiparkinsonian; nootropic; anticonvulsant; hepatotropic;
KW antipsoriatic; haemostatic; cytostatic; antilipemic; antiparasitic;
KW antihelmintic; antibacterial; virucide; protozoacide; fungicide;
KW cardiovascular disease; immune system; neurological; growth; development;
KW cell proliferation; viral; bacterial; fungal; parasitic; protozoan;
KW helminthic infection; transgenic; gene therapy; enzyme;
KW single nucleotide polymorphism; SNP.
XX
XX Homo sapiens.
OS
XX WO2004018641-A2.
XX
XX
XX 04-MAR-2004.
XX
XX 25-AUG-2003; 2003WO-US026635.
XX
XX 26-AUG-2002; 2002US-0406172P.
XX
XX 25-SEP-2002; 2002US-0413910P.
XX
XX 27-SEP-2002; 2002US-0414296P.

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PR 11-OCT-2002; 2002US-0417821P.
XX (INCY-) INCYTE CORP.
XX Baughn MR, Richardson TW, Marquis JP, Swarnakar A, Tang YT;
PI Becha SD, Emerling BM, Jin P, Wilson AD, Yue H, Gletzen KJ;
PI Chang H, Yang YG, Lee SY, Khare R, Elliott VS, Hafalia AJA;
PI Chawla NK, Ramkumar J, Gururajan R, Tribouley CM, Chien D, Tran UK;
PI Murage J;
XX
XX WPI; 2004-226830/21.
XX N-PSDB; ADK71920.
XX
XX New human kinases and phosphatases, useful for diagnosing, treating or
PT preventing atherosclerosis, hypertension, AIDS, allergy, multiple
PT sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, cancer
PT or hepatitis.
XX
XX Claim 1; SEQ ID NO 38; 347pp; English.
XX
XX The invention relates to a novel isolated polypeptide which is a human
XX kinase and phosphatase (KPP). The polypeptide of the invention
XX demonstrates cardiovascular, antiarteriosclerotic, hypotensive,
XX vasotropic, antiinflammatory, antianginal, anti-HIV, anti-allergic,
XX antiasthmatic, immunosuppressive, antithyroid, dermatological,
XX antidiabetic, nephrotropic, antigout, gastrointestinal, neuroprotective,
XX osteopachic, antiarthritic, uropathic, ophthalmological, antirheumatic,
XX antiparkinsonian, nootropic, anticonvulsant, hepatotropic, antipsoriatic,
XX haemostatic, cytostatic, antilipemic, antiparasitic, antihelminthic,
XX antibacterial, virucide, protozoacide and fungicide activities. The
XX kinase and phosphatase (KPP) polynucleotides, polypeptides, agonists and
XX antagonists may be useful for diagnosing, treating or preventing
XX disorders such as cardiovascular diseases, immune system disorders,
XX neurological disorders, disorders affecting growth and development, cell
XX proliferative disorders and viral, bacterial, fungal, parasitic,
XX protozoan or helminthic infections. Furthermore, the molecules of the
XX invention may be useful for creating transgenic animals to model human
XX disease and during gene therapy. The current sequence is that of a human
XX KPP protein of the invention.
XX
XX Sequence 486 AA;
XX
XX Query Match 100.0%; Score 1942; DB 8; Length 486;
XX Best Local Similarity 100.0%; Pred. No. 5.1e-178;
XX Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MYAMKYNKQOCIERDEVNVRFELEIQIEHVLVNLWYGFQDEDMFMVVDLLGGD 60
DB 118 MYAMKYNKQOCIERDEVNVRFELEIQIEHVLVNLWYGFQDEDMFMVVDLLGGD 177
QY 61 LRYHLOQNVQFSEDVRLVYICEMALDYLRGQHHIHRDVKPDNILLDERGHAHLTDFNI 120
DB 178 LRYHLOQNVQFSEDVRLVYICEMALDYLRGQHHIHRDVKPDNILLDERGHAHLTDFNI 237
QY 121 ATIIKDGERATALAGTKPMWPEIFHSFVNGGTGYSFEVDWWSVGMAYELLGRWPYDI 180
DB 238 ATIIKDGERATALAGTKPMWPEIFHSFVNGGTGYSFEVDWWSVGMAYELLGRWPYDI 297
QY 181 HSNNAVESLVQLFSTVSQVYPTWSKEMVALLKLLTVNPEHRLSSLDQVQAPALAGVL 240
DB 298 HSNNAVESLVQLFSTVSQVYPTWSKEMVALLKLLTVNPEHRLSSLDQVQAPALAGVL 357
QY 241 WDHLSEKRVPEGFPVPMKGRHLCDPTPELEMIKESRPLHKKKRLAKNKSRRNDSQS 300
DB 358 WDHLSEKRVPEGFPVPMKGRHLCDPTPELEMIKESRPLHKKKRLAKNKSRRNDSQS 417
QY 301 ENDYLODCLDAIQDDPVIINREKLKRSQDLPREPLPAPESRDAAEPVEDEERSALPMCG 360
DB 418 ENDYLODCLDAIQDDPVIINREKLKRSQDLPREPLPAPESRDAAEPVEDEERSALPMCG 477
QY 361 PICPSAGSG 369
DB 478 PICPSAGSG 486

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RESULT 5
AAM40592
ID AAM40592 standard; protein; 425 AA.
XX
XX AAM40592;
XX
XX 22-OCT-2001 (first entry)
XX
XX Human polypeptide SEQ ID NO 5523.
XX
XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
XX leukaemia.
XX
XX Homo sapiens.
XX
XX WO200153312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000WO-US034263.
XX
XX 23-DEC-1999; 99US-00471275.
XX
XX 21-JAN-2000; 2000US-00488725.
XX
XX 25-APR-2000; 2000US-00552317.
XX
XX 20-JUN-2000; 2000US-00598042.
XX
XX 19-JUL-2000; 2000US-00620312.
XX
XX 03-AUG-2000; 2000US-00653450.
XX
XX 14-SEP-2000; 2000US-00662191.
XX
XX 19-OCT-2000; 2000US-00693036.
XX
XX 29-NOV-2000; 2000US-00727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QH;
XX Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI; 2001-442253/47.
XX
XX N-PSDB; AAI59748.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders such
XX as central nervous system injuries.
XX
XX Example 2; SEQ ID NO 5523; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
XX encoded polypeptides (AAM38642-AAM42213) with nootropic,
XX immunosuppressant and cytostatic activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX localised neuropathies and central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX utilisation of the activities such as; Immune system suppression,
XX Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX assays for receptor activity, arthritis and inflammation, leukaemias and
XX C.N.S disorders. Note: The sequence data for this patent did not form
XX part of the printed specification
XX
XX Sequence 425 AA;
XX
XX Query Match 99.8%; Score 1939; DB 4; Length 425;
XX Best Local Similarity 99.7%; Pred. No. 8.2e-178;
XX Matches 368; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MYAMKYNKQCCIERDEVRNVFRELEILQIEHVFVNLWYSFQDEBDMFVVDLLGGD 60
Db 57 MYAMKYNKQCCIERDEVRNVFRELEILQIEHVFVNLWYSFQDEBDMFVVDLLGGD 116
QY 61 LRYHLQONVQFSEDVRLYICEMALADYLRGQHIHRDVKPNILLDERGHAHLTDFNI 120
Db 117 LRYHLQONVQFSEDVRLYICEMALADYLRGQHIHRDVKPNILLDERGHAHLTDFNI 176
QY 121 ATIIKGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 180
Db 177 ATIIKGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 236
QY 181 HSSNAVESLVQLFSTVSQVPTWSKEMVALLKRLTVNPEHRLSSLDQVQAAPALAGVL 240
Db 237 HSSNAVESLVQLFSTVSQVPTWSKEMVALLKRLTVNPEHRLSSLDQVQAAPALAGVL 296
QY 241 WDHLSEKRVPGFVFNKGRHCDPTPELEEMILESRLHKKKRLAKNKSRRDSSQS 300
Db 297 WDHLSEKRVPGFVFNKGRHCDPTPELEEMILESRLHKKKRLAKNKSRRDSSQS 356
QY 301 ENDYLQDCLDAIQDDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
Db 357 ENDYLQDCLDAIQDDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 416
QY 361 PICPSAGSG 369
Db 417 PICPSAGSG 425

RESULT 6
AAB65599 ID AAB65599 standard; protein; 419 AA.
AC AAB65599;
XX
DT 27-MAR-2001 (first entry)
XX
DE Novel protein kinase, SEQ ID NO: 124.
XX
KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
KW immunosuppressive; cardiac; renal; antiinflammatory; antiasthmatic;
KW dermatological; antidiabetic; antiinfertility; gene therapy; vaccine;
KW immune disorder; cardiovascular disease; neurodegenerative disease;
KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
KW inflammatory pelvic disease; multiple sclerosis; psoriasis.
OS Homo sapiens.
PN WO200073469-A2.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US014842.
XX
PR 28-MAY-1999; 99US-0136503P.
XX
PA (SUGEN-) SUGEN INC.
XX
PI Plowman GD, Martinez R, Whyte D, Sudersanam S;
XX
DR WPI; 2001-032161/04.
DR N-PSDB; AAF44624.
XX
PT Nucleic acids encoding kinase polypeptides, useful for diagnosing and
PT treating immune-related diseases and disorders, cardiovascular disease,
PT neurodegenerative diseases and/or cancers.
PS Claim 10; Fig 1; 310pp; English.
XX
CC The present sequence is a novel protein kinase. The novel protein kinases
CC and the nucleic acids that encode them may be used in the treatment and
CC diagnosis of diseases associated with inappropriate kinase expression
CC such as immune-related diseases and disorders, cardiovascular disease,

CC neurodegenerative diseases and/or cancers. The nucleic acids and
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays. The kinase polypeptides may be used as antigens in the production
CC of antibodies of kinase expression and activity. Anti-kinase antibodies
CC and kinase antagonists may also be used to down regulate kinase
CC expression and activity. Diseases related to kinase expression and
CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
CC disorders, complications of organ transplantation, myocardial infarction,
CC immune disorders, cardiomyopathies, strokes, renal failure, oxidative-
CC stress related disorders, chronic inflammatory bowel disease, chronic
CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
CC psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive
CC disorders
XX
SQ Sequence 419 AA;
Query Match 99.5%; Score 1933; DB 4; Length 419;
Best Local Similarity 99.7%; Pred. No. 3.1e-177;
Matches 368; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MYAMKYNKQCCIERDEVRNVFRELEILQIEHVFVNLWYSFQDEBDMFVVDLLGGD 60
Db 51 MYAMKYNKQCCIERDEVRNVFRELEILQIEHVFVNLWYSFQDEBDMFVVDLLGGD 110
QY 61 LRYHLQONVQFSEDVRLYICEMALADYLRGQHIHRDVKPNILLDERGHAHLTDFNI 120
Db 111 LRYHLQONVQFSEDVRLYICEMALADYLRGQHIHRDVKPNILLDERGHAHLTDFNI 170
QY 121 ATIIKGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 180
Db 171 ATIIKGERATALAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 230
QY 181 HSSNAVESLVQLFSTVSQVPTWSKEMVALLKRLTVNPEHRLSSLDQVQAAPALAGVL 240
Db 231 HSSNAVESLVQLFSTVSQVPTWSKEMVALLKRLTVNPEHRLSSLDQVQAAPALAGVL 290
QY 241 WDHLSEKRVPGFVFNKGRHCDPTPELEEMILESRLHKKKRLAKNKSRRDSSQS 300
Db 291 WDHLSEKRVPGFVFNKGRHCDPTPELEEMILESRLHKKKRLAKNKSRRDSSQS 350
QY 301 ENDYLQDCLDAIQDDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
Db 351 ENDYLQDCLDAIQDDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 410
QY 361 PICPSAGSG 369
Db 411 PICPSAGSG 419

RESULT 7
ADI29204 ID ADI29204 standard; protein; 419 AA.
XX
AC ADI29204;
XX
DT 22-APR-2004 (first entry)
XX
DE Human MARK3-associated protein #2.
XX
KW Human; antisense gene therapy; MARK3;
KW MAP/microtubule affinity-regulating kinase 3; cancer;
KW Alzheimer's disease; neurodegenerative disease;
KW hyperproliferative disorder; cytostatic.
XX
OS Homo sapiens.
PN US2003232771-A1.
XX
PD 18-DEC-2003.
XX
PF 17-JUN-2002; 2002US-00174319.
XX
PR 17-JUN-2002; 2002US-00174319.

XX	(ISIS-) ISIS PHARM INC.	XX	Human; NOVA; inflammatory disorder; demyelination disease; stroke;
PA		KW	renal disorder; infection; cardiomyopathy; atherosclerosis; acne;
XX		KW	hypertension; pancreatitis; Von Hippel-Lindau; endometriosis; fertility;
PI	Ward DT, Freier SM, Dobie KW;	KW	scleroderma; cirrhosis; inflammatory bowel disease; Crohn's disease;
XX		KW	haemophilia; autoimmune disease; allergy; AIDS;
DR	WPI; 2004-052188/05.	KW	graft versus host disease; Alzheimer's disease; arthritis; pain;
DR	N-PSDB; ADI29322.	KW	Parinson's disease; Huntington's disease; obesity; diabetes;
XX		KW	hair growth; hair loss; asthma; schizophrenia; glomerulonephritis;
PT	New antisense compound targeted to a nucleic acid molecule encoding	KW	lupus erythematosus; psoriasis; antidiabetic; anorectic; metabolic;
PT	microtubule-affinity-regulating kinases (MARK3), useful for modulating	KW	nootropic; neuroprotective; cytostatic; antibacterial; virucide;
PT	expression of MARK3 or for treating cancer or Alzheimer's disease.	KW	protozoacide; antiarteriosclerotic; hypotensive; cerebroprotective;
XX		KW	antiinflammatory; gynaecological; antiinfertility; dermatological;
PS	Disclosure; SEQ ID NO 124; 233pp; English.	KW	hepatotropic; haemostatic; immunosuppressive; anti-allergic;
XX		KW	antiarthritic; anticonvulsant; antiseborrhoeic; antiasthmatic;
CC	The invention relates to a compound comprising a sequence comprising 8-80	KW	neuroleptic; anti-HIV; analgesic; nephrotropic; antipsoriatic.
CC	base pairs (bp) targeted to a nucleic acid encoding MARK3	XX	
CC	(MAP/microtubule affinity-regulating kinase 3), that specifically	OS	Homo sapiens.
CC	hybridises with the nucleic acid encoding MARK3 and inhibits expression	XX	
CC	of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a	PN	WO200298917-A2.
CC	composition comprising the compound and a carrier or diluent, inhibiting	XX	
CC	the expression of MARK3 in cells or tissues, treating an animal having or	XX	12-DEC-2002.
CC	suspected of having a disease or condition associated with MARK3 and	XX	
CC	screening for an antisense compound. The antisense oligonucleotide is	XX	12-FEB-2002; 2002WO-US022049.
CC	useful for preparing a composition for treating hyperproliferative	PR	12-FEB-2001; 2001US-0268221P.
CC	disorder, particularly cancer and neurodegenerative diseases e.g.	PR	13-FEB-2001; 2001US-0268496P.
CC	Alzheimer's disease. The present sequence is a MARK3 associated protein	PR	14-FEB-2001; 2001US-0268646P.
CC	included in the figures but not mentioned anywhere else in the	PR	14-FEB-2001; 2001US-0268665P.
CC	specification.	PR	15-FEB-2001; 2001US-0269136P.
XX		PR	16-FEB-2001; 2001US-0269310P.
SQ	Sequence 419 AA;	PR	16-FEB-2001; 2001US-0269530P.
		PR	15-MAR-2001; 2001US-0276405P.
		PR	16-MAR-2001; 2001US-0276399P.
		PR	16-MAR-2001; 2001US-0276703P.
		PR	23-MAR-2001; 2001US-0278199P.
		PR	28-MAR-2001; 2001US-0279274P.
		PR	30-MAR-2001; 2001US-0280238P.
		PR	02-APR-2001; 2001US-0280899P.
		PR	08-AUG-2001; 2001US-0310797P.
		PR	14-AUG-2001; 2001US-0312284P.
		PR	14-SEP-2001; 2001US-0322294P.
		PR	14-SEP-2001; 2001US-0322295P.
		PR	18-OCT-2001; 2001US-0330293P.
		PR	31-OCT-2001; 2001US-0335104P.
		PR	31-OCT-2001; 2001US-0335109P.
		PR	21-NOV-2001; 2001US-0332127P.
		PR	28-NOV-2001; 2001US-0331772P.
		XX	
		PA	(CURA-) CURAGEN CORP.
		XX	
		PI	Guo X, Fernandes E, Li L, Kekuda R, Liu Y, Leite M, Spytek KA;
		PI	Ji W, Casman SJ, Boldog FL, Patturajan M, Vernet CAM, Ballinger RA;
		PI	Malvankar UM, Tchernev VT, Blalock AD, Gusev VV, Rastelli L;
		PI	Mezes PD, Ellerman K, Heyes M, Hermann JL, Shimkets RA, Ioime N;
		PI	Pena CEA, Shenoy SG, Taupier RJ, Gerlach V, Gorman L;
		XX	
		DR	WPI; 2003-148650/14.
		DR	N-PSDB; ACD20380.
		XX	
		PT	Novel NOVX polypeptide useful for identifying an agent that binds to the
		PT	polypeptide, and for treating cardiomyopathy, atherosclerosis,
		PT	hypertension, infertility, scleroderma, cirrhosis, and inflammatory bowel
		XX	disease.
		PS	Claim 1; Page 41; 566pp; English.
		XX	
		CC	The present invention relates to the isolation of novel human
		CC	polypeptides referred to as NOVX (NOVI-NOV37), variants of these
		CC	proteins, and the polynucleotide sequences encoding them. The NOVX
		CC	proteins of the invention share homology to various types of protein
		CC	families such as zinc finger-like proteins, enzymes, receptors, and
		CC	lipoproteins. The sequences of the invention may be useful in the

CC manufacture of a medicament for treating a syndrome associated with a
 CC human disease. For example they can be used to treat inflammatory
 CC disorders, demyelination disease, renal disorders, infections,
 CC cardiomyopathy, atherosclerosis, hypertension, stroke, pancreatitis, Von
 CC Hippel-Lindau, endometriosis, fertility, scleroderma, cirrhosis,
 CC inflammatory bowel disease, Crohn's disease, haemophilia, autoimmune
 CC diseases, allergies, graft versus host disease, Alzheimer's disease,
 CC arthritis, Parkinson's disease, Huntington's disease, obesity, diabetes,
 CC acne, hair growth/loss, asthma, schizophrenia, AIDS, pain,
 CC glomerulonephritis, lupus erythematosus, and psoriasis. ABO14984-ABO15039
 CC represent the NOVX polypeptides of the invention. Note: SEQ ID Nos 113-
 CC 460 are known sequences used for homology purposes

XX
 SQ Sequence 488 AA;

Query Match 99.3%; Score 1927.5; DB 6; Length 488;

Best Local Similarity 99.5%; Pred. No. 1.3e-176; Indels 1; Gaps 1;
 Matches 368; Conservative 0; Mismatches 1;

Qy 1 MYAMKYNKQCCIERDEVRNVFRELEILQIEHVLVNLWYSFQDEDMFVVDLLGGD 60
 Db 119 MYAMKYNKQCCIERDEVRNVFRELEILQIEHVLVNLWYSFQDEDMFVVDLLGGD 178
 Qy 61 LRYHLQONVQFSEDTVRLYICEMALADYLRGQHIHRDVKPNILDERGHAHLTD FNI 120
 Db 179 LRYHLQONVQFSEDTVRLYICEMALADYLRGQHIHRDVKPNILDERGHAHLTD FNI 238
 Qy 121 ATTIKGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
 Db 239 ATTIKGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 298
 Qy 181 HSSNAVESLVQLFSTVSQVPTWSEKMWALLRK-LLTVPNPEHRLSLQDVQAAPALAGV 239
 Db 299 HSSNAVESLVQLFSTVSQVPTWSEKMWALLRK-LLTVPNPEHRLSLQDVQAAPALAGV 358
 Qy 240 LWDHLSKRVPEPGVPNKGRLHCDPTFELEEMILESRLHKKKRLAKNKS RDNRS DSSQ 299
 Db 359 LWDHLSKRVPEPGVPNKGRLHCDPTFELEEMILESRLHKKKRLAKNKS RDNRS DSSQ 418
 Qy 300 SENDYLODCLDAIQODFVIFNREKLRKSQDLPREPLPAPESRDAEPVEDEAERSALPMC 359
 Db 419 SENDYLODCLDAIQODFVIFNREKLRKSQDLPREPLPAPESRDAEPVEDEAERSALPMC 478
 Qy 360 GPICPSAGSG 369
 Db 479 GPICPSAGSG 488

RESULT 9
 AAM38806

ID AAM38806 standard; protein; 419 AA.

XX
 AC AAM38806;

XX
 DT 22-OCT-2001 (first entry)

XX
 DE Human polypeptide SEQ ID NO 1951.

XX Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW Chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.

XX
 OS Homo sapiens.

XX
 PN W0200153312-A1.

XX
 PD 26-JUL-2001.

XX
 PF 26-DEC-2000; 2000WO-US034263.

XX

PR 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-00488725.
 PR 25-APR-2000; 2000US-00552317.
 PR 20-JUN-2000; 2000US-00598042.
 PR 19-JUL-2000; 2000US-00620312.
 PR 03-AUG-2000; 2000US-00653450.
 PR 14-SEP-2000; 2000US-00662191.
 PR 13-OCT-2000; 2000US-00693036.
 PR 29-NOV-2000; 2000US-00727344.
 XX (HYSE-) HYSEQ INC.
 PA
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PI Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI; 2001-442253/47.
 DR N-PSDB; AAI57962.

XX Novel nucleic acids and polypeptides, useful for treating disorders such
 as central nervous system injuries.

PS Example 3; SEQ ID NO 1951; 10078pp; English.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
 CC encoded polypeptides (AAM38642-AAM42213) with neurotropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders. Note: The sequence data for this patent did not form
 CC part of the printed specification

XX Sequence 419 AA;

Query Match 99.1%; Score 1924; DB 4; Length 419;

Best Local Similarity 99.5%; Pred. No. 2.3e-176; Indels 0; Gaps 0;
 Matches 367; Conservative 0; Mismatches 2;

Qy 1 MYAMKYNKQCCIERDEVRNVFRELEILQIEHVLVNLWYSFQDEDMFVVDLLGGD 60
 Db 51 MYAMKYNKQCCIERDEVRNVFRELEILQIEHVLVNLWYSFQDEDMFVVDLLGGD 110
 Qy 61 LRYHLQONVQFSEDTVRLYICEMALADYLRGQHIHRDVKPNILDERGHAHLTD FNI 120
 Db 111 LRYHLQONVQFSEDTVRLYICEMALADYLRGQHIHRDVKPNILDERGHAHLTD FNI 170
 Qy 121 ATTIKGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVMAYELLRGWRPYDI 180
 Db 171 ATTIKGERATAGTKPYMAPEIFHSFVNVVTGYSFEVDWWSVGVMAYELLRGWRPYDI 230
 Qy 181 HSSNAVESLVQLFSTVSQVPTWSEKMWALLRK-LLTVPNPEHRLSLQDVQAAPALAGV 240
 Db 231 HSSNAVESLVQLFSTVSQVPTWSEKMWALLRK-LLTVPNPEHRLSLQDVQAAPALAGV 290
 Qy 241 WDHLSKRVPEPGVPNKGRLHCDPTFELEEMILESRLHKKKRLAKNKS RDNRS DSSQ 300
 Db 291 WDHLSKRVPEPGVPNKGRLHCDPTFELEEMILESRLHKKKRLAKNKS RDNRS DSSQ 350
 Qy 301 ENDYLODCLDAIQODFVIFNREKLRKSQDLPREPLPAPESRDAEPVEDEAERSALPMC 360
 Db 351 ENDYLODCLDAIQODFVIFNREKLRKSQDLPREPLPAPESRDAEPVEDEAERSALPMC 410
 Qy 361 PICPSAGSG 369
 Db 411 PICPSAGSG 419

PS	Claim 6; Page 207-209; 290pp; English.	
XX	ABL39691 to ABL39818 represent novel human nucleic acid sequences	
CC	(NS) can have cytotostatic, osteopathic, gynaecological, neuroprotective,	
CC	antirheumatic, antiarthritic, antispasmodic, ophthalmological, virucide,	
CC	vasotropic, antiarteriosclerotic, antiinflammatory, dermatological,	
CC	anorectic, muscular, anti-HIV, antinfertility, cardiovascular,	
CC	anticoagulant, antifibrinolytic, hypotension, antidiabetic, cardiac,	
CC	immunomodulator, anticonvulsant, antidiabetic, tranquiliser, antiulcer,	
CC	antidepressant, gastrointestinal, neuroleptic, cerebroprotective,	
CC	nootropic and contraceptive activities. The NS can be used in vaccines and	
CC	gene therapy and antisense therapy. Nucleic acids, expression vectors and	
CC	antibodies from the present invention can be used for treating and	
CC	diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative	
CC	diseases, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis,	
CC	cataracts, restenosis, atherosclerosis, inflammation, skin disorders,	
CC	glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascular	
CC	disease, coagulation disease, ischaemia, hypertension, asthma, immune	
CC	disease, epilepsy, angina, neurodegeneration, diabetes, anxiety,	
CC	depression, schizophrenia, viral disease, gastric ulcers, stroke,	
CC	Alzheimer's disease and as a contraceptive	
XX	Sequence 713 AA;	
SQ	Query Match 95.6%; Score 1856.5; DB 5; Length 713;	
	Best Local Similarity 92.5%; Pred. No. 1.6e-169;	
	Matches 358; Conservative 0; Mismatches 6; Indels 23; Gaps 1;	
QY	1 MYAMKYNKQCCIERDEVNVPFRELQIEIHVFLVNLWYSFQDEDMFVVDDLGGD 60	
DB	160 MYAMKYNKQCCIERDEVNVPFRELQIEIHVFLVNLWYSFQDEDMFVVDDLGGD 219	
QY	61 LRYHLQONVQFSEDVRLVICEMALDYLRCQHIIHRDVKPDNIIILDERGHAHLTDFNI 120	
DB	220 LRYHLQONVQFSEDVRLVICEMALDYLRCQHIIHRDVKPDNIIILDERGHAHLTDFNI 279	
QY	121 ATIKDGERATAGTKPYMAPEIFHSFVNGGTGYSFVDWMSVGMAYELLRGWRPYDI 180	
DB	280 ATIKDGERATAGTKPYMAPEIFHSFVNGGTGYSFVDWMSVGMAYELLRGWRPYDI 339	
QY	181 HSSNAVESLVQLFSTVSQVPTWSEKEMVALLKLTVPNPEHRLSSLDQVQAAPALAGVL 240	
DB	340 HSSNAVESLVQLFSTVSQVPTWSEKEMVALLKLTVPNPEHRLSSLDQVQAAPALAGVL 399	
QY	241 WDHLSEKRVPGVPVKNKGRHLCDPTPELEEMILESPLHKKKRLAKNKSNDNRSSQS 300	
DB	400 WDHLSEKRVPGVPVKNKGRHLCDPTPELEEMILESPLHKKKRLAKNKSNDNRSSQS 459	
QY	301 -----ENDYLODCLDAIQODFVIFNREKLRKSODLPREPLPA 337	
DB	460 APRSKSPSTQSGSWALASSGWNEDYLODCLDAIQODFVIFNREKLRKSODLPREPLPA 519	
QY	338 PESRDAAEPEDEAERSALPMCGPICP 364	
DB	520 PESRDAAEPEDEAERSALPMCGPIVP 546	
RESULT 12		
AAO17708		
ID	AAO17708 standard; protein; 364 AA.	
XX	AAO17708;	
AC		
XX		
DT	20-AUG-2002 (first entry)	
XX	Human serine-threonine protein kinase.	
XX		
KW	Human; serine-threonine protein kinase; cancer; diabetes; obesity;	
KW	central nervous system disorder; inflammation; gene therapy; COPD;	
KW	neuroprotective; antiparkinsonian; cerebroprotective; cytostatic;	
KW	antidiabetic; antiallergic; antiaesthetic; antidepressant; anorectic;	
KW	antiinflammatory; immunomodulator; chronic obstructive pulmonary disease;	
enzyme.		
OS	Homo sapiens.	
PN	WO200233056-A2.	
XX	25-APR-2002.	
PD		
XX	15-OCT-2001; 2001WO-EP011892.	
PF		
XX	16-OCT-2000; 2000US-0240097P.	
PR	30-JUL-2001; 2001US-0308096P.	
XX	(FARB) BAYER AG.	
PA		
XX	Koehler RH;	
PI		
XX	WPI; 2002-435534/46.	
DR	N-PSDB; AAL46714.	
XX	New human serine-threonine protein kinase and encoding polynucleotides,	
PT	useful for diagnosing, treating and preventing central nervous system	
PT	disorders (e.g. stroke), diabetes, or cancers (e.g. leukemia).	
XX	Claim 25; Fig 2; 135pp; English.	
PS		
XX	The present invention provides the protein and coding sequences of a	
CC	human serine-threonine protein kinase. The sequences can be used in the	
CC	diagnosis, treatment and prevention of cancers (e.g. leukemia, lymphoma	
CC	or melanoma), CNS disorders (e.g. Parkinson's disease, stroke, or	
CC	traumatic brain injury), diabetes, eating disorders (e.g. obesity,	
CC	anorexia, or cachexia), allergies, anaphylaxis, asthma, inflammation and	
CC	chronic obstructive pulmonary disease (COPD). The present sequence is the	
CC	protein of the invention	
XX	Sequence 364 AA;	
SQ	Query Match 95.0%; Score 1845; DB 5; Length 364;	
	Best Local Similarity 99.7%; Pred. No. 7.7e-169;	
	Matches 351; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MYAMKYNKQCCIERDEVNVPFRELQIEIHVFLVNLWYSFQDEDMFVVDDLGGD 60	
DB	13 MYAMKYNKQCCIERDEVNVPFRELQIEIHVFLVNLWYSFQDEDMFVVDDLGGD 72	
QY	61 LRYHLQONVQFSEDVRLVICEMALDYLRCQHIIHRDVKPDNIIILDERGHAHLTDFNI 120	
DB	73 LRYHLQONVQFSEDVRLVICEMALDYLRCQHIIHRDVKPDNIIILDERGHAHLTDFNI 132	
QY	121 ATIKDGERATAGTKPYMAPEIFHSFVNGGTGYSFVDWMSVGMAYELLRGWRPYDI 180	
DB	133 ATIKDGERATAGTKPYMAPEIFHSFVNGGTGYSFVDWMSVGMAYELLRGWRPYDI 192	
QY	181 HSSNAVESLVQLFSTVSQVPTWSEKEMVALLKLTVPNPEHRLSSLDQVQAAPALAGVL 240	
DB	193 HSSNAVESLVQLFSTVSQVPTWSEKEMVALLKLTVPNPEHRLSSLDQVQAAPALAGVL 252	
QY	241 WDHLSEKRVPGVPVKNKGRHLCDPTPELEEMILESPLHKKKRLAKNKSNDNRSSQS 300	
DB	253 WDHLSEKRVPGVPVKNKGRHLCDPTPELEEMILESPLHKKKRLAKNKSNDNRSSQS 312	
QY	301 ENDYLODCLDAIQODFVIFNREKLRKSODLPREPLPAESRDAAEPEDEAE 352	
DB	313 ENDYLODCLDAIQODFVIFNREKLRKSODLPREPLPAESRDAAEPEDEAE 364	
RESULT 13		
AAE24141		
ID	AAE24141 standard; protein; 485 AA.	
XX	AAE24141;	
XX		
DT	23-SEP-2002 (first entry)	

XX Human kinase (PKIN)-12 protein.

XX Human; kinase; PKIN; cancer; immune system disorder; atherosclerosis;

XX acquired immune deficiency syndrome; AIDS; Addison's disease; allergy;

XX asthma; multiple sclerosis; psoriasis; arteriosclerosis; cirrhosis;

XX development; hepatitis; cardiovascular; hypertension; drug screening;

XX myocardial infarction; Goodpasture's syndrome; lipid disorder; growth;

XX fatty liver; Gaucher's disease; Niemann-Pick's disease; anorectic;

XX hypercholesterolaemia; obesity; gene therapy; cytostatic; anti-HIV;

XX neuroprotective; hepatotropic; hypotensive; cardiant; nephrotropic;

XX hyperlipidaemia; enzyme.

OS Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..24

XX Protein 25..485

XX Domain /note= "Human mature kinase (PKIN)-12"

XX Domain /note= "Protein kinase domain"

XX Domain /note= "Protein kinase domain"

XX Domain /note= "Eukaryotic protein kinase domain"

XX Domain /note= "Protein kinase domain"

XX WO200233099-A2.

XX 25-APR-2002.

XX 20-OCT-2001; 2001WO-US047728.

XX 20-OCT-2000; 2000US-0242410P.

XX 03-OCT-2000; 2000US-0244068P.

XX 09-NOV-2000; 2000US-0247672P.

XX 16-NOV-2000; 2000US-0249565P.

XX 22-NOV-2000; 2000US-0252730P.

XX 01-DEC-2000; 2000US-0250807P.

XX (INCY-) INCYTE GENOMICS INC.

XX Gururajan R, Baughn MR, Walia NK, Elliott VS, Xu Y, Arvizu C;

XX Yao MG, Ramkumar J, Ding L, Tang YT, Hafalia AJA, Nguyen DB;

XX Gandhi AR, Lu Y, Yue H, Burford N, Bandman O, Tribouley CM, Lal PG;

XX Recipon SA, Lu DAM, Borowsky ML, Thornton M, Swarnaker A;

XX Thangavelu K, Khan FA, Ison CH;

XX WPI; 2002-454603/48.

XX N-PSDB; AAD38855.

XX New human kinase polypeptide, for diagnosing, preventing and treating

XX cancer, immune system disorders, growth and development disorders,

XX cardiovascular disorders and lipid disorders.

XX Claim 1; Page 160-161; 210pp; English.

XX The invention relates human kinases (PKIN) and their corresponding

XX nucleic acid sequences. PKIN and its DNA are useful for diagnosing,

XX treating and preventing cancer, an immune system disorder (e.g., acquired

XX immune deficiency syndrome (AIDS), Addison's disease, allergy, asthma,

XX atherosclerosis, multiple sclerosis, psoriasis), disorders affecting

XX growth and development (e.g., arteriosclerosis, cirrhosis, hepatitis),

XX cardiovascular disorder (e.g., hypertension, myocardial infarction,

XX Goodpasture's syndrome), and a lipid disorder (e.g., fatty liver,

XX Gaucher's disease, Niemann-Pick's disease, hypercholesterolaemia,

XX hyperlipidaemia, obesity), and for assessing the effects of exogenous

XX compounds. Anti-PKIN antibody is useful in a diagnostic test for a

XX condition or a disease associated with the expression of PKIN in a

XX biological sample. A composition comprising PKIN or an agonist or

CC antagonist of PKIN is useful for treating a disease or condition

CC associated with decreased or increased expression of functional PKIN.

CC PKIN is useful in a number of drug screening techniques and to analyse

CC the proteome of a tissue or cell type. PKIN DNA is useful for creating

CC knockin humanised animals or transgenic animals to model human diseases,

CC and in somatic or germline gene therapy. The present sequence is human

CC PKIN protein

XX Sequence 485 AA;

SQ Query Match 94.1%; Score 1827.5; DB 5; Length 485;

Best Local Similarity 95.4%; Pred. No. 5.7e-167;

Matches 352; Conservative 1; Mismatches 15; Indels 1; Gaps 1;

QY 1 MYAMKYNKQOCIERDEVNVRNPRELEILQIEHVFVNLWYSFQDEEDMFVVDLLGGD 60

DB 118 MYAMKYNKQOCIERDEVNVRNPRELEILQIEHVFVNLWYSFQDEEDMFVVDLLGGD 177

QY 61 LRYHLQONVQFSEDVRLYICEMALALDYLRQOHIIHRDVKPDNILLDERGHAHLTDENI 120

DB 178 LRYHLQONVQFSEDVRLYICEMALALDYLRQOHIIHRDVKPDNILLDERGHAHLTDENI 237

QY 121 ATIIKDGERTALAGTKPYMAPEIFHPSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 180

DB 238 ATIIKDGERTALAGTKPYMAPEIFHPSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 297

QY 181 HSSNAVESLVQLFSTVSQVYPTWSKEMVALLRKLLTVNPEHRLSSLDQVQAPALAGVL 240

DB 298 HSSNAVESLVQLFSTVSQVYPTWSKEMVALLRKLLTVNPEHRLSSLDQVQAPALAGVL 357

QY 241 WDHLSEKRVGFGVFNKGRHLHCDPTFELEEMLESRLPKKKKRLAKNKRDNSSDSQS 300

DB 358 WDHLSEKRVGFGVFNKGRHLHCDPTFELEEMLESRLPKKKKRLAKNKRDNSSDSQS 417

QY 301 ENDYLQDCLDALIQDDFVFNREKLKRSODLREPUPAPESRDAAPVEDEAERSALPMCG 360

DB 418 ENDYLQDCLDALIQDDFVFNREKLKRSODLREPUPA-LSPGMLRSLWRTRTLRLPMCG 476

QY 361 PICPSAGSG 369

DB 477 PICPSAGSG 485

RESULT 14

ABB84300

ID ABB84300 standard; protein; 399 AA.

XX

AC ABB84300;

XX

DT 12-NOV-2002 (first entry)

XX

DE Murine serine/threonine protein kinase subfamily-related protein.

XX

KW Serine/threonine protein kinase subfamily; chromosome 10; enzyme; murine;

KW cytostatic; gene therapy; drug screening; tissue typing; prostate; lung;

KW pharmacogenomic; brain.

XX

OS Mus musculus.

XX

PN WO200259288-A2.

XX

PD 01-AUG-2002.

XX

PF 15-JAN-2002; 2002WO-US000930.

XX

PR 23-JAN-2001; 2001US-0263162P.

PR 29-MAR-2001; 2001US-00819607.

XX

PA (PEKE) PE CORP NY.

XX

PI Beasley EM, Ye J, Yan C, Ketchum KA, Di Francesco V;

XX

XX WPI; 2002-599781/64.

XX New peptides related to serine/threonine protein kinase subfamily, useful
PT for treating disorders associated with abnormal expression of kinase in
PT prostate, lungs and brain, in drug screening assays and pharmacogenomic
PT analysis.
XX
PS Disclosure; Fig 2B; 86pp; English.
XX
XX This invention describes a novel serine/threonine protein kinase
CC subfamily-associated protein isolated from human chromosome 10 which has
CC cytostatic activity and can be used for gene therapy. The products of the
CC invention are useful in substantial and specific assays related to
CC functional information of the peptide sequences, to raise antibodies or
CC to elicit immune response, as reagents in assays to determine the levels
CC of protein in biological fluids, and as markers for tissues where the
CC corresponding protein is expressed. The peptides and antibodies are
CC useful in drug screening assays, tissue typing and pharmacogenomic
CC analysis. They are also useful in treating disorders associated with the
CC absence of, inappropriate, or unwanted expression of kinase protein in
CC prostate, lungs or brain. The nucleic acid molecules are useful for
CC probes, primers and chemical intermediates in biological assays, for
CC constructing recombinant vectors, expressing antigenic portions of the
CC protein. The peptide and nucleic acid sequences are useful as models for
CC the development of human therapeutic targets, aid in the identification
CC of therapeutic proteins and serve as targets for the development of human
CC therapeutic agents that modulate kinase activity in cells and tissues
CC that express the kinase. The host cells are useful in producing a kinase
CC protein or peptide, and non-human transgenic animals. This sequence
CC represents a murine serine/threonine protein kinase subfamily-associated
CC protein described in the disclosure of the invention
XX
SQ Sequence 399 AA;

Query Match 92.0%; Score 1786.5; DB 5; Length 399;
Best Local Similarity 92.4%; Pred. No. 3.8e-163;
Matches 341; Conservative 10; Mismatches 17; Indels 1; Gaps 1;
QY 1 MYAMKYNKQOCIERDEVNRFRELEIQEIEHVFVNLWYSFQDEDMFVVDLLGGD 60
DB 31 MYAMKYNKQOCIERDEVNRFRELEIQEIEHVFVNLWYSFQDEDMFVVDLLGGD 90
QY 61 LRYHLOQNVQFSEDVRLYICEMALDYLRLGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
DB 91 LRYHLOQNVQFSEDVRLYICEMALDYLRLGQHIIHRDVKPDNILLDERGHAHLTDFNI 150
QY 121 ATTIKDGGERATAGTKPYMAPBIFHSFVNGGTGYSFEVDWWSVGMAYELLRGWRPYDI 180
DB 151 ATTIKDGGERATAGTKPYMAPBIFHSFVNGGTGYSFEVDWWSVGMAYELLRGWRPYDI 210
QY 181 HSSNAVESLVQLFSTVSQVPTWSEKEMVALLRKLITVNPPEHRLSLIQDVAAPALAGVL 240
DB 211 HSSNAVESLVQLFSTVSQVPTWSEKEMVALLRKLITVNPPEHRLSLIQDVAAPALAGVL 270
QY 241 WDHLSEKRVPGFVFNKGRHLCDPTPELEEMILESRLPHKKKRLAKNKSRRDSSQS 300
DB 271 WDHLSEKRVPGFVFNKGRHLCDPTPELEEMILESRLPHKKKRLAKNKSRRDSSQS 330
QY 301 ENDYLOQCLDAIQDQFVFNREKLKRSQDLPREPLPAPESRDAEPVED-EAERSALPMC 359
DB 331 ENDYLOQCLDAIQDQFVFNREKLKRSQELMSEPPPGPETSMDTSTADSEAPALPMC 390
QY 360 GPICPSAGS 368
DB 391 GSICPSSGS 399
RESULT 15
AA017709
XX ID AA017709 standard; protein; 488 AA.
XX AC AA017709;
XX DT 20-AUG-2002 (first entry)

XX Murine serine-threonine protein kinase.
XX Human; serine-threonine protein kinase; cancer; diabetes; obesity;
KW central nervous system disorder; inflammation; gene therapy; COPD;
KW neuroprotective; antiparkinsonian; cerebroprotective; cytostatic;
KW antidiabetic; antiallergic; antiasthmatic; antidepressant; anorectic;
KW antiinflammatory; immunomodulator; chronic obstructive pulmonary disease;
KW enzyme.
XX
XX Mus musculus.
OS
XX WO200233056-A2.
PN
XX 25-APR-2002.
PD
XX 15-OCT-2001; 2001WO-EP011892.
PF
XX 16-OCT-2000; 2000US-0240097P.
PR
XX 30-JUL-2001; 2001US-0308096P.
PR
XX (FARB) BAYER AG.
PA
XX Koehler RH;
XX WPI; 2002-435534/46.
XX New human serine-threonine protein kinase and encoding polynucleotides,
PT useful for diagnosing, treating and preventing central nervous system
PT disorders (e.g. stroke), diabetes, or cancers (e.g. leukemia).
XX
PS Disclosure; Fig 3; 135pp; English.
XX
CC The present invention provides the protein and coding sequences of a
CC human serine-threonine protein kinase. The sequences can be used in the
CC diagnosis, treatment and prevention of cancers (e.g. leukaemia, lymphoma
CC or melanoma), CNS disorders (e.g. Parkinson's disease, stroke, or
CC traumatic brain injury), diabetes, eating disorders (e.g. obesity,
CC anorexia, or cachexia), allergies, anaphylaxis, asthma, inflammation and
CC chronic obstructive pulmonary disease (COPD). The present sequence is a
CC murine serine-threonine protein kinase
XX
SQ Sequence 488 AA;
Query Match 92.0%; Score 1786.5; DB 5; Length 488;
Best Local Similarity 92.4%; Pred. No. 5.1e-163;
Matches 341; Conservative 10; Mismatches 17; Indels 1; Gaps 1;
QY 1 MYAMKYNKQOCIERDEVNRFRELEIQEIEHVFVNLWYSFQDEDMFVVDLLGGD 60
DB 119 MYAMKYNKQOCIERDEVNRFRELEIQEIEHVFVNLWYSFQDEDMFVVDLLGGD 178
QY 61 LRYHLOQNVQFSEDVRLYICEMALDYLRLGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
DB 179 LRYHLOQNVQFSEDVRLYICEMALDYLRLGQHIIHRDVKPDNILLDERGHAHLTDFNI 238
QY 121 ATTIKDGGERATAGTKPYMAPBIFHSFVNGGTGYSFEVDWWSVGMAYELLRGWRPYDI 180
DB 239 ATTIKDGGERATAGTKPYMAPBIFHSFVNGGTGYSFEVDWWSVGMAYELLRGWRPYDI 298
QY 181 HSSNAVESLVQLFSTVSQVPTWSEKEMVALLRKLITVNPPEHRLSLIQDVAAPALAGVL 240
DB 299 HSSNAVESLVQLFSTVSQVPTWSEKEMVALLRKLITVNPPEHRLSLIQDVAAPALAGVL 358
QY 241 WDHLSEKRVPGFVFNKGRHLCDPTPELEEMILESRLPHKKKRLAKNKSRRDSSQS 300
DB 359 WDHLSEKRVPGFVFNKGRHLCDPTPELEEMILESRLPHKKKRLAKNKSRRDSSQS 418
QY 301 ENDYLOQCLDAIQDQFVFNREKLKRSQDLPREPLPAPESRDAEPVED-EAERSALPMC 359
DB 419 ENDYLOQCLDAIQDQFVFNREKLKRSQELMSEPPPGPETSMDTSTADSEAPALPMC 478
QY 360 GPICPSAGS 368

Db 479 GSICPSSGS 487

Search completed: May 9, 2006, 10:48:29
Job time : 189 secs

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OM protein - protein search, using sw model

Run on: May 9, 2006, 10:45:55 ; Search time 27 Seconds
(without alignments)
1129.901 Million cell updates/sec

Title: US-10-633-631-2
Perfect score: 1942
Sequence: 1 MYAMKYNKQCCIERDEVN.....EAERSALPMCGPICPSAGSG 369

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfilesi.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1942	100.0	369	2	US-09-819-607-2
2	1942	100.0	419	2	US-09-799-875-14
3	1873.5	96.5	368	2	US-09-819-607-5
4	1786.5	92.0	399	2	US-09-819-607-4
5	1710	88.1	384	2	US-09-801-876B-6
6	1710	88.1	384	2	US-10-254-869-6
7	1710	88.1	384	2	US-10-667-442-6
8	1265.5	65.2	403	2	US-09-801-876B-5
9	1265.5	65.2	403	2	US-10-254-869-5
10	1265.5	65.2	403	2	US-10-667-442-5
11	1250	64.4	404	2	US-09-801-876B-4
12	1250	64.4	404	2	US-10-254-869-4
13	1250	64.4	404	2	US-10-667-442-4
14	1146.5	59.0	396	2	US-09-841-683-11
15	1146.5	59.0	396	2	US-10-620-845-11
16	1142	58.8	407	2	US-09-841-683-9
17	1142	58.8	407	2	US-10-620-845-9
18	1137.5	58.6	396	2	US-09-801-876B-2
19	1137.5	58.6	396	2	US-10-254-869-2
20	1137.5	58.6	396	2	US-10-667-442-2
21	1078.5	55.5	316	2	US-09-801-876B-7
22	1078.5	55.5	316	2	US-10-254-869-7
23	1078.5	55.5	316	2	US-10-667-442-7
24	754	38.8	347	2	US-09-801-876B-8
25	754	38.8	347	2	US-10-254-869-8
26	754	38.8	347	2	US-10-667-442-8
27	709	36.5	225	2	US-09-841-683-5

28	709	36.5	225	2	US-10-620-845-5	Sequence 5, Appli
29	709	36.5	236	2	US-09-841-683-7	Sequence 7, Appli
30	709	36.5	236	2	US-10-620-845-7	Sequence 7, Appli
31	453	23.3	380	2	US-09-487-558B-402	Sequence 402, App
32	444	22.9	740	2	US-09-538-092-1178	Sequence 1178, Ap
33	444	22.9	740	2	US-09-771-161A-265	Sequence 265, App
34	444	22.9	740	2	US-09-771-161A-265	Sequence 265, App
35	425.5	21.9	824	2	US-09-487-558B-312	Sequence 312, App
36	424	21.8	597	1	US-08-313-274-2	Sequence 2, Appli
37	424	21.8	655	2	US-09-949-016-11676	Sequence 11676, A
38	423	21.8	260	1	US-07-857-224B-7	Sequence 7, Appli
39	419	21.6	398	2	US-09-538-092-501	Sequence 501, App
40	419	21.6	398	2	US-09-487-558B-404	Sequence 404, App
41	417	21.5	397	2	US-09-487-558B-400	Sequence 400, App
42	416	21.4	480	2	US-09-091-058-2	Sequence 2, Appli
43	416	21.4	480	2	US-09-590-740-2	Sequence 2, Appli
44	416	21.4	480	2	US-09-538-092-1053	Sequence 1053, Ap
45	416	21.4	480	2	US-09-526-043-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-819-607-2
; Sequence 2, Application US/09819607
; Patent No. 6686176
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001078
; CURRENT APPLICATION NUMBER: US/09/819,607
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Human
US-09-819-607-2

Query Match		100.0%;	Score 1942;	DB 2;	Length 369;
Best Local Similarity		100.0%;	Pred. No. 2.9e-159;		
Matches 369;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MYAMKYNKQCCIERDEVN	VFRELEIQEIEHVFVLNLMWYSFQDEEDFMVVDLLGGD	60	
DB	1	MYAMKYNKQCCIERDEVN	VFRELEIQEIEHVFVLNLMWYSFQDEEDFMVVDLLGGD	60	
QY	61	LYYHLOONVQSFEDTVRLYICEMALDYLRCGHIHROVKPDNIILLDERGHAHLTDENI	120		
DB	61	LYYHLOONVQSFEDTVRLYICEMALDYLRCGHIHROVKPDNIILLDERGHAHLTDENI	120		
QY	121	ATIIKDGERTALAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI	180		
DB	121	ATIIKDGERTALAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI	180		
QY	181	HSSNAVESLVQFSTVSQVYPTWSEKEMVALLRKLTVMPEHRLSLQDVQAAAPALAGVL	240		
DB	181	HSSNAVESLVQFSTVSQVYPTWSEKEMVALLRKLTVMPEHRLSLQDVQAAAPALAGVL	240		
QY	241	WDHLSEKRVPGFVFNKGRHLCDPTPELEEMILESPLHKKKRLAKNKSNDNRSSQS	300		
DB	241	WDHLSEKRVPGFVFNKGRHLCDPTPELEEMILESPLHKKKRLAKNKSNDNRSSQS	300		
QY	301	ENDYLDQCLDADQQDFVIFNREKLKESQDLPREPLPAPESRDAAEPVEDEAERSALPMCG	360		
DB	301	ENDYLDQCLDADQQDFVIFNREKLKESQDLPREPLPAPESRDAAEPVEDEAERSALPMCG	360		
QY	361	PICPSAGSG 369			

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Db          361 PICPSAGSG 369

RESULT 2
US-09-799-875-14
; Sequence 14, Application US/09799875
; Patent No. 6638721
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 35800/209996
; CURRENT APPLICATION NUMBER: US/09/799,875
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/182,059
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/659,287
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-875-14

Query Match      100.0%; Score 1942; DB 2; Length 419;
Best Local Similarity 100.0%; Pred. No. 3.4e-159;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYAMKYNKQOCIERDEVNVPFRELILQIEIHVFLVNLWYSFQDEDMFMVVDLLGGD 60
DB 51 MYAMKYNKQOCIERDEVNVPFRELILQIEIHVFLVNLWYSFQDEDMFMVVDLLGGD 110
QY 61 LRYHLQONVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
DB 111 LRYHLQONVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 170
QY 121 ATIIKDGERTALAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 180
DB 171 ATIIKDGERTALAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 230
QY 181 HSSNAVESLVQLFSTVSQVYPTWMSKEMVALLRKLLTVNPEHRLSSLODQVQAPALAGVL 240
DB 231 HSSNAVESLVQLFSTVSQVYPTWMSKEMVALLRKLLTVNPEHRLSSLODQVQAPALAGVL 290
QY 241 WDHLSEKRVEPGFPVKNKGRLLHCDPTFELEEMILESRLHKKKRLAKNKSNDNRDSSQS 300
DB 291 WDHLSEKRVEPGFPVKNKGRLLHCDPTFELEEMILESRLHKKKRLAKNKSNDNRDSSQS 350
QY 301 ENDYLODCLDAIQODFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
DB 351 ENDYLODCLDAIQODFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 410
QY 361 PICPSAGSG 369
DB 411 PICPSAGSG 419

RESULT 3
US-09-819-607-5
; Sequence 5, Application US/09819607
; Patent No. 6686176
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001078
; CURRENT APPLICATION NUMBER: US/09/819,607
; CURRENT FILING DATE: 2001-03-29

; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-819-607-4

Query Match      92.0%; Score 1786.5; DB 2; Length 399;
Best Local Similarity 92.4%; Pred. No. 8.1e-146;
Matches 341; Conservative 10; Mismatches 17; Indels 1; Gaps 1;

QY 1 MYAMKYNKQOCIERDEVNVPFRELILQIEIHVFLVNLWYSFQDEDMFMVVDLLGGD 60
DB 31 MYAMKYNKQOCIERDEVNVPFRELILQIEIHVFLVNLWYSFQDEDMFMVVDLLGGD 90
QY 61 LRYHLQONVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 120
DB 91 LRYHLQONVQFSEDTVRLYICEMALALDYLRGQHIIHRDVKPDNILLDERGHAHLTDFNI 150
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Qy 121 ATIKDGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWVGVGMAYELLRGWRPYDI 180
Db 151 ATIKDGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWVGVGMAYELLRGWRPYDI 210
Qy 181 HSSNAVESLVQLFSTVSQVPTWSEKEMVALLRKLLTVNPEHRLSSLODVOAAPALAGVL 240
Db 211 HSSNAVESLVQLFSTVSQVPTWSEKEMVALLRKLLTVNPEHRLSSLODVOAAPALAGVL 270
Qy 241 WDHLSEKRVPGFVFNKGRHLHCDPTFELEEMILESRLPKKKKRLAKNKRDNRSRSSQS 300
Db 271 WDDLSEKRVPGFVFNKGRHLHCDPTFELEEMILESRLPKKKKRLAKNKRDNRSRSSQS 330
Qy 301 ENDYLODCLDAIQODFVIFNREKLKRSQDLPRPLPAPESRDAAPVED-EABRSALPMC 359
Db 331 ENDYLODCLDAIQODFVIFNREKLKRSQELMSEPPPGPETSMTDSTADSEAPTLPMC 390
Qy 360 GPICPSNGS 368
Db 391 GSICPSSGS 399
RESULT 5
US-09-801-876B-6
; Sequence 6, Application US/09801876B
; Patent No. 6492155
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001160
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Mus Musculus
US-09-801-876B-6

Query Match 88.1%; Score 1710; DB 2; Length 384;
Best Local Similarity 95.0%; Pred. No. 3e-139;
Matches 325; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
Qy 1 MYAMKYNKQOCIERDEVNVRFRELEILOEIEHVFVLNLMYSFQDEEDMFVVDLLGGD 60
Db 43 MYAMKYNKQOCIERDEVNVRFRELEILOEIEHVFVLNLMYSFQDEEDMFVVDLLGGD 102
Qy 61 LRYHLQONVQFSEDVRLYICEMALDYLGRQHIHRDVKPDNIILDERGHAHLTDfNI 120
Db 103 LRYHLQONVQFSEDVRLYICEMALDYLRSQHIHRDVKPDNIILDEGHAHLTDfNI 162
Qy 121 ATIKDGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWVGVGMAYELLRGWRPYDI 180
Db 163 ATIKDGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWVGVGMAYELLRGWRPYDI 222
Qy 181 HSSNAVESLVQLFSTVSQVPTWSEKEMVALLRKLLTVNPEHRLSSLODVOAAPALAGVL 240
Db 223 HSSNAVESLVQLFSTVSQVPTWSEKEMVALLRKLLTVNPEHRLSSLODVOAAPALAGVL 282
Qy 241 WDHLSEKRVPGFVFNKGRHLHCDPTFELEEMILESRLPKKKKRLAKNKRDNRSRSSQS 300
Db 283 WDDLSEKRVPGFVFNKGRHLHCDPTFELEEMILESRLPKKKKRLAKNKRDNRSRSSQS 342
Qy 301 ENDYLODCLDAIQODFVIFNREKLKRSQDLPRPLPAPESRD 342
Db 343 ENDYLODCLDAIQODFVIFNREKLKRSQELMSEPPPGPETS 384

RESULT 6
US-10-254-869-6
; Sequence 6, Application US/10254869

; Patent No. 6653117
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001160DIV
; CURRENT APPLICATION NUMBER: US/10/254,869
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-254-869-6
Query Match 88.1%; Score 1710; DB 2; Length 384;
Best Local Similarity 95.0%; Pred. No. 3e-139;
Matches 325; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
Qy 1 MYAMKYNKQOCIERDEVNVRFRELEILOEIEHVFVLNLMYSFQDEEDMFVVDLLGGD 60
Db 43 MYAMKYNKQOCIERDEVNVRFRELEILOEIEHVFVLNLMYSFQDEEDMFVVDLLGGD 102
Qy 61 LRYHLQONVQFSEDVRLYICEMALDYLGRQHIHRDVKPDNIILDERGHAHLTDfNI 120
Db 103 LRYHLQONVQFSEDVRLYICEMALDYLRSQHIHRDVKPDNIILDEGHAHLTDfNI 162
Qy 121 ATIKDGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWVGVGMAYELLRGWRPYDI 180
Db 163 ATIKDGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWVGVGMAYELLRGWRPYDI 222
Qy 181 HSSNAVESLVQLFSTVSQVPTWSEKEMVALLRKLLTVNPEHRLSSLODVOAAPALAGVL 240
Db 223 HSSNAVESLVQLFSTVSQVPTWSEKEMVALLRKLLTVNPEHRLSSLODVOAAPALAGVL 282
Qy 241 WDHLSEKRVPGFVFNKGRHLHCDPTFELEEMILESRLPKKKKRLAKNKRDNRSRSSQS 300
Db 283 WDDLSEKRVPGFVFNKGRHLHCDPTFELEEMILESRLPKKKKRLAKNKRDNRSRSSQS 342
Qy 301 ENDYLODCLDAIQODFVIFNREKLKRSQDLPRPLPAPESRD 342
Db 343 ENDYLODCLDAIQODFVIFNREKLKRSQELMSEPPPGPETS 384

RESULT 7
US-10-667-442-6
; Sequence 6, Application US/10667442
; Patent No. 6821765
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001160DIV II
; CURRENT APPLICATION NUMBER: US/10/667,442
; CURRENT FILING DATE: 2003-09-23
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-667-442-6
Query Match 88.1%; Score 1710; DB 2; Length 384;
Best Local Similarity 95.0%; Pred. No. 3e-139;
Matches 325; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
Qy 1 MYAMKYNKQOCIERDEVNVRFRELEILOEIEHVFVLNLMYSFQDEEDMFVVDLLGGD 60
Db 43 MYAMKYNKQOCIERDEVNVRFRELEILOEIEHVFVLNLMYSFQDEEDMFVVDLLGGD 102

Db 48 MYAMKYNKQCCI-ERDEVNVPFRELQIMQGLEHPPFLVNLWYSFQDEDMFMVVDLLGG 107
 QY 61 LRYHLQONVQFSDTVRLVICEMALADYLRQGHIIHRDVKPNILLDERGHAHLTDFNI 120
 Db 108 LRYHLQONVHFTGTVKLYICELALALEYLQRYHIIHRDIKPNILLDEHGHVHTDFNI 167
 QY 121 ATIIKDGGERATAGTKPYMAPEIFHSFVNGGTGYSEFVDWMSVGMAYELLRGWRPYDI 180
 Db 168 ATVVKGAERASSMAGTKPYMAPEVQVYMDRGPYSPVDMWSLGTAYELLRGWRPYEI 227
 QY 181 HSSNAVESLVOLFSTVSQVYPTWSKEMVALLKLTVPNPEHRLSSLODQVQAPALAGVL 240
 Db 228 HSVPIDEILNMPKVERVHYSSTWCKGMVALLKLTQKDPESRVSSLHDIQSPYIADWN 287
 QY 241 WDHLSEKRVPEPGVPNKGRLHCDPTFELEEMILESRLHKKKRLAKNKSNDNSRDSQS 300
 Db 288 WDAVFKALMPGVPNKGRLNCDPTFELEEMILESRLHKKKRLAKNKSNDNSRDSQS 347
 QY 301 ENDYLQDCLDAIQODFVIFNREKLKRSQ 328
 Db 348 -NGHLQCLQLETVREKLEKLRQQ 374

RESULT 11
 US-09-801-876B-4
 ; Sequence 4, Application US/09801876B
 ; Patent No. 6492155
 ; GENERAL INFORMATION:
 ; APPLICANT: YE, Jane et al
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: CL001160
 ; CURRENT APPLICATION NUMBER: US/09/801,876B
 ; CURRENT FILING DATE: 2001-03-09
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 404
 ; TYPE: PRP
 ; ORGANISM: Mus Musculus
 US-09-801-876B-4

Query Match 64.4%; Score 1250; DB 2; Length 404;
 Best Local Similarity 68.7%; Pred. No. 1.5e-99;
 Matches 226; Conservative 55; Mismatches 46; Indels 2; Gaps 2;

QY 1 MYAMKYNKQCCI-ERDEVNVPFRELQIMQGLEHPPFLVNLWYSFQDEDMFMVVDLLGG 59
 Db 48 MYAMKYNKQCKQERDEVNVPFRELQIMQGLEHPPFLVNLWYSFQDEDMFMVVDLLGG 107
 QY 60 DLYHLLQONVQFSDTVRLVICEMALADYLRQGHIIHRDVKPNILLDERGHAHLTDFN 119
 Db 108 DLYHLLQONVHFTGTVKLYICELALALEYLQRYHIIHRDIKPNILLDEHGHVHTDFN 167
 QY 120 ATIIKDGGERATAGTKPYMAPEIFHSFVNGGTGYSEFVDWMSVGMAYELLRGWRPYD 179
 Db 168 IATVLKGEKASSMAGTKPYMAPEVQVYMDRGPYSPVDMWSLGTAYELLRGWRPYE 227
 QY 180 HSSNAVESLVOLFSTVSQVYPTWSKEMVALLKLTVPNPEHRLSSLODQVQAPALAGV 239
 Db 228 IHSATPIDEILNMPKVERVHYSSTWCEGMVSLKLTQKDPESRLSSLRDIQSMYTLADM 287
 QY 240 WDHLSEKRVPEPGVPNKGRLHCDPTFELEEMILESRLHKKKRLAKNKSNDNSRDSQ 299
 Db 288 NWDVFEKALMPGVPNKGRLNCDPTFELEEMILESRLHKKKRLAKNKSNDNSRDSQ 347
 QY 300 SENDYLQDCLDAIQODFVIFNREKLKRSQ 328
 Db 348 L-NGHLQCLQLETVRKGEFIIFNREKLRRQQ 375

RESULT 12

US-10-254-869-4
 ; Sequence 4, Application US/10254869
 ; Patent No. 6653117
 ; GENERAL INFORMATION:
 ; APPLICANT: YE, Jane et al
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: CL001160DIV
 ; CURRENT APPLICATION NUMBER: US/10/254,869
 ; CURRENT FILING DATE: 2002-09-26
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 404
 ; TYPE: PRP
 ; ORGANISM: Mus Musculus
 US-10-254-869-4

Query Match 64.4%; Score 1250; DB 2; Length 404;
 Best Local Similarity 68.7%; Pred. No. 1.5e-99;
 Matches 226; Conservative 55; Mismatches 46; Indels 2; Gaps 2;

QY 1 MYAMKYNKQCCI-ERDEVNVPFRELQIMQGLEHPPFLVNLWYSFQDEDMFMVVDLLGG 59
 Db 48 MYAMKYNKQCKQERDEVNVPFRELQIMQGLEHPPFLVNLWYSFQDEDMFMVVDLLGG 107
 QY 60 DLYHLLQONVQFSDTVRLVICEMALADYLRQGHIIHRDVKPNILLDERGHAHLTDFN 119
 Db 108 DLYHLLQONVHFTGTVKLYICELALALEYLQRYHIIHRDIKPNILLDEHGHVHTDFN 167
 QY 120 IATIIKDGGERATAGTKPYMAPEIFHSFVNGGTGYSEFVDWMSVGMAYELLRGWRPYD 179
 Db 168 IATVLKGEKASSMAGTKPYMAPEVQVYMDRGPYSPVDMWSLGTAYELLRGWRPYE 227
 QY 180 HSSNAVESLVOLFSTVSQVYPTWSKEMVALLKLTVPNPEHRLSSLODQVQAPALAGV 239
 Db 228 IHSATPIDEILNMPKVERVHYSSTWCEGMVSLKLTQKDPESRLSSLRDIQSMYTLADM 287
 QY 240 WDHLSEKRVPEPGVPNKGRLHCDPTFELEEMILESRLHKKKRLAKNKSNDNSRDSQ 299
 Db 288 NWDVFEKALMPGVPNKGRLNCDPTFELEEMILESRLHKKKRLAKNKSNDNSRDSQ 347
 QY 300 SENDYLQDCLDAIQODFVIFNREKLKRSQ 328
 Db 348 L-NGHLQCLQLETVRKGEFIIFNREKLRRQQ 375

RESULT 13
 US-10-667-442-4
 ; Sequence 4, Application US/10667442
 ; Patent No. 6821765
 ; GENERAL INFORMATION:
 ; APPLICANT: YE, Jane et al
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: CL001160DIV II
 ; CURRENT APPLICATION NUMBER: US/10/667,442
 ; CURRENT FILING DATE: 2003-09-23
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 404
 ; TYPE: PRP
 ; ORGANISM: Mus Musculus
 US-10-667-442-4

Query Match 64.4%; Score 1250; DB 2; Length 404;
 Best Local Similarity 68.7%; Pred. No. 1.5e-99;
 Matches 226; Conservative 55; Mismatches 46; Indels 2; Gaps 2;

QY 1 MYAMKYNKQCCI-ERDEVNVPFRELQIMQGLEHPPFLVNLWYSFQDEDMFMVVDLLGG 59

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Db      48 MYAMKYNKQCKQVERDEVNVERELQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGG 107
QY      60 LRYHLQONVQFSEDVRLYICEMALADYLRGQHIHRDVKPDNILLDERGHAHLTDFN 119
Db      108 LRYHLQONVHFTEGTVKLYICELALALEYLRQYHIHRDIKPDNILLDEHGHVHTDFN 167
QY      120 IATIIKGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGMAYELLRGWRPYD 179
Db      168 IATVLKSEKASSMAGTKPYMAPEVQVYVGGPGYSYPVDMWSLGTATAYELLRGWRPYE 227
QY      180 IHSNNAVESLVLQFSTVSQYVPTWSKEMVALLRKLLTVNPEHRLSSLODVOAAPALAGV 239
Db      228 IHSATFIDELNNKFKVERHYHSTWCEGMVSLKULLTKDPESSLRLDIOQMTYLDAM 287
QY      240 LWDHLSEKRVPEPGFVPNKGRLHCDPTFELEEMILESRLPHKKKKRLAKNKSNDNSRDSQ 299
Db      288 NWDVAFKALMPCGFVNKGRNLCDPTFELEEMILESPLHKKKKRLAKHRSRSTKDSQP 347
QY      300 SENDYLODCLDALQODFVIFNREKLRSQ 328
Db      348 L-NGHLQOCLTETVRKEFIIFNREKLRRQ 375
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RESULT 14

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US-09-841-683-11
; Sequence 11, Application US/09841683
; Patent No. 6617147
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. 6617147el Human Kinase Proteins and Polynucleotides Encoding
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/09/841,683
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 396
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-841-683-11
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Query Match      59.0%; Score 1146.5; DB 2; Length 396;
Best Local Similarity 63.1%; Pred. No. 1.2e-90;
Matches 219; Conservative 47; Mismatches 72; Indels 9; Gaps 3;

QY      1 MYAMKYNKQCKQIERDEVNVPRELEIQEIEHVFVLNWLWYSFQDEEDMFVVDLLGG 60
Db      48 MYAMKYNKQCKVERNEVRNVFKEIQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGG 107
QY      61 LRYHLQONVQFSDVRLYICEMALADYLRGQHIHRDVKPDNILLDERGHAHLTDFNI 120
Db      108 LRYHLQONVHFKEETVKLFICELVMDLYLQNRHHRDVKPDNILLDEHGHVHTDFNI 167
QY      121 ATIIKGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGMAYELLRGWRPYDI 180
Db      168 AAMLPRETQITTMAGTKPYMAPEMFSS--RKGAGYSFAVDWWSLGTATAYELLRGRRPYHI 225
QY      181 HSNNAVESLVLQFSTVSQYVPTWSKEMVALLRKLLTVNPEHRLSSLODVOAAPALAGVL 240
Db      226 RSTSSKEIVHTFTTWTVPYPSAWSEQMVSLLKLEPNPDQRFQSLSDVQFPYMNNDIN 285
QY      241 WDHLSKRVPEPGFVPNKGRLHCDPTFELEEMILESRLPHKKKKRLAKNKSNDNSRDSQ 300
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Db      286 WDAVFQKRLIPGFIENKGRNLCDPTFELEEMILESPLHKKKKRLAKKEKDMRKCDSSQT 345
QY      301 ENDYLODCLDALQODFVIFNREKL-----KRSQDLPRELPAPESRD 342
Db      346 --CLLQEHLDVSQKBEFIIFNREKVNDRFNKQPNLALEQTKDPOGED 390

RESULT 15
US-10-620-845-11
; Sequence 11, Application US/10620845
; Patent No. 6908758
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: No. 6908758el Human Kinase Proteins and Polynucleotides Encoding
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/10/620,845
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/841,683
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 396
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-620-845-11
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Query Match      59.0%; Score 1146.5; DB 2; Length 396;
Best Local Similarity 63.1%; Pred. No. 1.2e-90;
Matches 219; Conservative 47; Mismatches 72; Indels 9; Gaps 3;

QY      1 MYAMKYNKQCKQIERDEVNVPRELEIQEIEHVFVLNWLWYSFQDEEDMFVVDLLGG 60
Db      48 MYAMKYNKQCKVERNEVRNVFKEIQIMQGLEHPFLVNLWYSFQDEEDMFVVDLLGG 107
QY      61 LRYHLQONVQFSEDVRLYICEMALADYLRGQHIHRDVKPDNILLDERGHAHLTDFNI 120
Db      108 LRYHLQONVHFKEETVKLFICELVMDLYLQNRHHRDVKPDNILLDEHGHVHTDFNI 167
QY      121 ATIIKGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGMAYELLRGWRPYDI 180
Db      168 AAMLPRETQITTMAGTKPYMAPEMFSS--RKAGAGYSFAVDWWSLGTATAYELLRGRRPYHI 225
QY      181 HSNNAVESLVLQFSTVSQYVPTWSKEMVALLRKLLTVNPEHRLSSLODVOAAPALAGVL 240
Db      226 RSTSSKEIVHTFTTVPYPSAWSEQMVSLLKLEPNPDQRFQSLSDVQFPYMNNDIN 285
QY      241 WDHLSKRVPEPGFVPNKGRLHCDPTFELEEMILESRLPHKKKKRLAKNKSNDNSRDSQ 300
Db      286 WDAVFQKRLIPGFIENKGRNLCDPTFELEEMILESPLHKKKKRLAKKEKDMRKCDSSQT 345
QY      301 ENDYLODCLDALQODFVIFNREKL-----KRSQDLPRELPAPESRD 342
Db      346 --CLLQEHLDVSQKBEFIIFNREKVNDRFNKQPNLALEQTKDPOGED 390
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Search completed: May 9, 2006, 10:48:16
Job time : 27 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 9, 2006, 10:47:54 ; Search time 78 Seconds
(without alignments)
1976.654 Million cell updates/sec

Title: US-10-633-631-2

Perfect score: 1942

Sequence: 1 MYAMKYNKQCCIERDEVRN.....EAERSALPMCGPICPSAGSG 369

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA_Main:*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
 - 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
 - 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
 - 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
 - 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
 - 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1942	100.0	369	3	US-09-819-607-2
2	1942	100.0	369	4	US-10-074-978A-155
3	1942	100.0	369	4	US-10-633-631-2
4	1942	100.0	369	4	US-10-408-765A-2411
5	1942	100.0	419	3	US-09-799-875-14
6	1942	100.0	419	4	US-10-303-664A-6
7	1942	100.0	419	4	US-10-649-156-14
8	1942	100.0	486	4	US-10-618-941-75
9	1927.5	99.3	488	4	US-10-074-978A-18
10	1873.5	96.5	368	3	US-09-819-607-5
11	1873.5	96.5	368	4	US-10-074-978A-156
12	1873.5	96.5	368	4	US-10-633-631-5
13	1827.5	94.1	485	4	US-10-415-011-12
14	1786.5	92.0	399	3	US-09-819-607-4
15	1786.5	92.0	399	4	US-10-633-631-4
16	1786.5	92.0	488	4	US-10-074-978A-154
17	1710	88.1	384	3	US-09-801-876B-6
18	1710	88.1	384	4	US-10-254-869-6
19	1710	88.1	384	4	US-10-667-442-6
20	1710	88.1	384	5	US-10-962-625-6
21	1576	81.2	375	4	US-10-168-582-12
22	1265.5	65.2	403	3	US-09-801-876B-5
23	1265.5	65.2	403	4	US-10-254-869-5
24	1265.5	65.2	403	4	US-10-667-442-5
25	1265.5	65.2	403	5	US-10-962-625-5
26	1265.5	65.2	414	4	US-10-354-358-36
27	1265.5	65.2	414	4	US-10-074-978A-157

28	1265.5	65.2	414	5	US-10-723-860-415	Sequence 415, App
29	1260.5	64.9	414	4	US-10-074-978A-158	Sequence 158, App
30	1250	64.4	404	3	US-09-801-876B-4	Sequence 4, Appli
31	1250	64.4	404	4	US-10-254-869-4	Sequence 4, Appli
32	1250	64.4	404	4	US-10-667-442-4	Sequence 4, Appli
33	1250	64.4	404	5	US-10-962-625-4	Sequence 4, Appli
34	1249.5	64.3	364	4	US-10-052-586-572	Sequence 572, App
35	1249.5	64.3	364	4	US-10-174-590-572	Sequence 572, App
36	1249.5	64.3	364	4	US-10-176-758-572	Sequence 572, App
37	1249.5	64.3	364	4	US-10-175-737-572	Sequence 572, App
38	1249.5	64.3	364	4	US-10-174-581-572	Sequence 572, App
39	1249.5	64.3	364	4	US-10-176-483-572	Sequence 572, App
40	1249.5	64.3	364	4	US-10-176-749-572	Sequence 572, App
41	1249.5	64.3	364	4	US-10-176-914-572	Sequence 572, App
42	1249.5	64.3	364	4	US-10-176-915-572	Sequence 572, App
43	1249.5	64.3	364	4	US-10-173-706-572	Sequence 572, App
44	1249.5	64.3	364	4	US-10-175-738-572	Sequence 572, App
45	1249.5	64.3	364	4	US-10-175-752-572	Sequence 572, App

ALIGNMENTS

RESULT 1

US-09-819-607-2
; Sequence 2, Application US/09819607
; Publication No. US20030022337A1
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001078
; CURRENT APPLICATION NUMBER: US/09/819,607
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Human
; US-09-819-607-2

Query Match	100.0%;	Score 1942;	DB 3;	Length 369;
Best Local Similarity	100.0%;	Pred. No. 1.4e-143;		
Matches	369;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	MYAMKYNKQCCIERDEVRNVFRELEILQBIIEHVLVNLWYSFQDEEDMFVVDLLGGD	60	
Db	1	MYAMKYNKQCCIERDEVRNVFRELEILQBIIEHVLVNLWYSFQDEEDMFVVDLLGGD	60	
Qy	61	LRVHLOONVQFSDTVRLYICEMALDYLGRGOHIIHRDVKPNILDERGHAHLTD FNI	120	
Db	61	LRVHLOONVQFSDTVRLYICEMALDYLGRGOHIIHRDVKPNILDERGHAHLTD FNI	120	
Qy	121	ATTIKDGERATAGTKPYNAPEIFHSFVNGGTGYSFEVDWWSVGNVAYELLRGWRPYDI	180	
Db	121	ATTIKDGERATAGTKPYNAPEIFHSFVNGGTGYSFEVDWWSVGNVAYELLRGWRPYDI	180	
Qy	181	HSSNAVESLVQLFSTVSQVPTWSEKEMVALLRKLTVPNPEHRLSSIQDVOAAPALAGVL	240	
Db	181	HSSNAVESLVQLFSTVSQVPTWSEKEMVALLRKLTVPNPEHRLSSIQDVOAAPALAGVL	240	
Qy	241	WDHLSEKRVPGFVPNKGRLHCDPTPELEEMILESRLHKKKRLAKNKRSDNRSDSSQS	300	
Db	241	WDHLSEKRVPGFVPNKGRLHCDPTPELEEMILESRLHKKKRLAKNKRSDNRSDSSQS	300	
Qy	301	ENDYLODCLDAIQODFVFNREKLKRSQDLPREPLPAPERKDAAEPEVEAERSALPMCG	360	
Db	301	ENDYLODCLDAIQODFVFNREKLKRSQDLPREPLPAPERKDAAEPEVEAERSALPMCG	360	
Qy	361	PICPSAGSG	369	

Db 361 PICPSAGSG 369

RESULT 2

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US-10-074-978A-155
; Sequence 155, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
; APPLICANT: Leite, Mario
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Fernandes, Elma
; APPLICANT: Li, Li
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Liu, Xiahong
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Patturajan, Meera
; APPLICANT: Bialock, Angela
; APPLICANT: Ballinger, Robert
; APPLICANT: Vernet, Corine
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter S
; APPLICANT: Ellerman, Karen
; APPLICANT: Heyes, Melvin P
; APPLICANT: Herrman, John
; APPLICANT: Pena, Carol E A
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Moore, No. US20040010119A11e
; APPLICANT: Shenoy, Suresh
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, Dave
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-269
; CURRENT APPLICATION NUMBER: US/10/074, 978A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: 60/268, 221
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/335, 109
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/312, 284
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/268, 496
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/276, 703
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/330, 293
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/322, 127
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/280, 899
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/310, 797
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/268, 646
; PRIOR FILING DATE: 2001-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 155
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-074-978A-155
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Query Match 100.0%; Score 1942; DB 4; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.4e-143;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYAMKYMKNKQOCIERDEVNVRNPRELEIQEIEHVFVNLNWLWYSFQDEEDMFVVDLLLGSD 60
Db 1 MYAMKYMKNKQOCIERDEVNVRNPRELEIQEIEHVFVNLNWLWYSFQDEEDMFVVDLLLGSD 60
QY 61 LRYHLQNNVQFSEDTVRLYICEMALALDYLRQGHIIHRDVKPDNILLDERGHAHLTDFNI 120
Db 61 LRYHLQNNVQFSEDTVRLYICEMALALDYLRQGHIIHRDVKPDNILLDERGHAHLTDFNI 120
QY 121 ATIIKGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 180
Db 121 ATIIKGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 180
QY 181 HSSNAVESLVQLFSTVSVQYVPTWSEKEMVALLRKLLTVNPEHRLSSLSQDVQAAPALAGVL 240
Db 181 HSSNAVESLVQLFSTVSVQYVPTWSEKEMVALLRKLLTVNPEHRLSSLSQDVQAAPALAGVL 240
QY 241 WDHLSEKRVPGFVFNKGRGLHCDPTFELBEMILESRLHKKKRLAKNKRDNRSRDSQS 300
Db 241 WDHLSEKRVPGFVFNKGRGLHCDPTFELBEMILESRLHKKKRLAKNKRDNRSRDSQS 300
QY 301 ENDYLQDCLDAIQDFVIFNRREKLRSQDLPREPLPAPESRDAABPVEDEAERSALPMCG 360
Db 301 ENDYLQDCLDAIQDFVIFNRREKLRSQDLPREPLPAPESRDAABPVEDEAERSALPMCG 360
QY 361 PICPSAGSG 369
Db 361 PICPSAGSG 369

RESULT 3
US-10-633-631-2
; Sequence 2, Application US/10633631
; Publication No. US20040067568A1
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001078DIV
; CURRENT APPLICATION NUMBER: US/10/633, 631
; CURRENT FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-633-631-2
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Query Match 100.0%; Score 1942; DB 4; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.4e-143;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYAMKYMKNKQOCIERDEVNVRNPRELEIQEIEHVFVNLNWLWYSFQDEEDMFVVDLLLGSD 60
Db 1 MYAMKYMKNKQOCIERDEVNVRNPRELEIQEIEHVFVNLNWLWYSFQDEEDMFVVDLLLGSD 60
QY 61 LRYHLQNNVQFSEDTVRLYICEMALALDYLRQGHIIHRDVKPDNILLDERGHAHLTDFNI 120
Db 61 LRYHLQNNVQFSEDTVRLYICEMALALDYLRQGHIIHRDVKPDNILLDERGHAHLTDFNI 120
QY 121 ATIIKGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 180
Db 121 ATIIKGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWMSVGMAYELLRGWRPYDI 180
QY 181 HSSNAVESLVQLFSTVSVQYVPTWSEKEMVALLRKLLTVNPEHRLSSLSQDVQAAPALAGVL 240
Db 181 HSSNAVESLVQLFSTVSVQYVPTWSEKEMVALLRKLLTVNPEHRLSSLSQDVQAAPALAGVL 240
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Qy 241 WDHLSEKRVPGFVPNKGRLHCDPTFELEMILESRLPHKKKRLAKNKRSDNSRDSQS 300
Db 241 WDHLSEKRVPGFVPNKGRLHCDPTFELEMILESRLPHKKKRLAKNKRSDNSRDSQS 300
Qy 301 ENDYLQDCLDAIQODFVIFNREKLKRSQDLPREPLPAPESRDAEPVEDEAERSALPMCG 360
Db 301 ENDYLQDCLDAIQODFVIFNREKLKRSQDLPREPLPAPESRDAEPVEDEAERSALPMCG 360
Qy 361 PICPSAGSG 369
Db 361 PICPSAGSG 369

RESULT 4
US-10-408-765A-2411
; Sequence 2411, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2411
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2411
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Query Match 100.0%; Score 1942; DB 4; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.4e-143;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MYAMKYNKQCCIERDEVNRNVFRELEILQIEHVFVNLWYSFQDEEDMFVVDLLGGD 60
Qy 61 LRYHLQNVQFSEDVRLYICEMALDYLRGQHIHRDVKPDNILLDERGHAHLTD FNI 120
Db 61 LRYHLQNVQFSEDVRLYICEMALDYLRGQHIHRDVKPDNILLDERGHAHLTD FNI 120
Qy 121 ATIIKGERATALAGTKPYNAPEIFHSFVNGGTGYSFEVDWWSVGVNAYELLRGWRPYDI 180
Db 121 ATIIKGERATALAGTKPYNAPEIFHSFVNGGTGYSFEVDWWSVGVNAYELLRGWRPYDI 180
Qy 181 HSSNAVESLVQLFSTVSQVQVPTWSKEMVALLRKLLTVNPEHRLSSLDQVQAAPALAGVL 240
Db 181 HSSNAVESLVQLFSTVSQVQVPTWSKEMVALLRKLLTVNPEHRLSSLDQVQAAPALAGVL 240
Qy 241 WDHLSEKRVPGFVPNKGRLHCDPTFELEMILESRLPHKKKRLAKNKRSDNSRDSQS 300
Db 241 WDHLSEKRVPGFVPNKGRLHCDPTFELEMILESRLPHKKKRLAKNKRSDNSRDSQS 300
Qy 301 ENDYLQDCLDAIQODFVIFNREKLKRSQDLPREPLPAPESRDAEPVEDEAERSALPMCG 360
Db 301 ENDYLQDCLDAIQODFVIFNREKLKRSQDLPREPLPAPESRDAEPVEDEAERSALPMCG 360
Qy 361 PICPSAGSG 369
Db 361 PICPSAGSG 369

RESULT 5
US-09-799-875-14
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; Sequence 14, Application US/09799875
; Patent No. US20020034780A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: No. US20020034780A1el Human Protein Kinases and Uses
; FILE REFERENCE: 35800/209996
; CURRENT APPLICATION NUMBER: US/09/799,875
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/182,059
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/659,287
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-875-14

Query Match 100.0%; Score 1942; DB 3; Length 419;
Best Local Similarity 100.0%; Pred. No. 1.7e-143;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYAMKYNKQCCIERDEVNRNVFRELEILQIEHVFVNLWYSFQDEEDMFVVDLLGGD 60
Db 51 MYAMKYNKQCCIERDEVNRNVFRELEILQIEHVFVNLWYSFQDEEDMFVVDLLGGD 110
Qy 61 LRYHLQNVQFSEDVRLYICEMALDYLRGQHIHRDVKPDNILLDERGHAHLTD FNI 120
Db 111 LRYHLQNVQFSEDVRLYICEMALDYLRGQHIHRDVKPDNILLDERGHAHLTD FNI 170
Qy 121 ATIIKGERATALAGTKPYNAPEIFHSFVNGGTGYSFEVDWWSVGVNAYELLRGWRPYDI 180
Db 171 ATIIKGERATALAGTKPYNAPEIFHSFVNGGTGYSFEVDWWSVGVNAYELLRGWRPYDI 230
Qy 181 HSSNAVESLVQLFSTVSQVQVPTWSKEMVALLRKLLTVNPEHRLSSLDQVQAAPALAGVL 240
Db 231 HSSNAVESLVQLFSTVSQVQVPTWSKEMVALLRKLLTVNPEHRLSSLDQVQAAPALAGVL 290
Qy 241 WDHLSEKRVPGFVPNKGRLHCDPTFELEMILESRLPHKKKRLAKNKRSDNSRDSQS 300
Db 291 WDHLSEKRVPGFVPNKGRLHCDPTFELEMILESRLPHKKKRLAKNKRSDNSRDSQS 350
Qy 301 ENDYLQDCLDAIQODFVIFNREKLKRSQDLPREPLPAPESRDAEPVEDEAERSALPMCG 360
Db 351 ENDYLQDCLDAIQODFVIFNREKLKRSQDLPREPLPAPESRDAEPVEDEAERSALPMCG 410
Qy 361 PICPSAGSG 369
Db 411 PICPSAGSG 419

RESULT 6
US-10-303-664A-6
; Sequence 6, Application US/10303664A
; Publication No. US20030153018A1
; GENERAL INFORMATION:
; APPLICANT: Hunter, John Joseph
; APPLICANT: Williamson, Mark W.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Teai, Fong-Ying
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CANCER USING 2192, 2193, 6568, 8895, 9138, 9217, 9609,
; TITLE OF INVENTION: 9857, 9882, 10025, 20657, 21163, 25848, 25968, 32603, 32670,
; TITLE OF INVENTION: 33794, 54476 and 94710
; FILE REFERENCE: MPI2001-290F3R(M)
; CURRENT APPLICATION NUMBER: US/10/303,664A
; CURRENT FILING DATE: 2002-11-25
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Qy 301 ENDYLDCLDAIQDFVIFNREKLKRSQDLPREPLPAPESRDAAPVEDEAERSALPMC 360
Db 418 ENDYLDCLDAIQDFVIFNREKLKRSQDLPREPLPAPESRDAAPVEDEAERSALPMC 477
Qy 361 PICPSAGSG 369
Db 478 PICPSAGSG 486

RESULT 9

US-10-074-978A-18
; Sequence 18, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
; APPLICANT: Leite, Mario
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Fernandes, Elma
; APPLICANT: Li, Li
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Liu, Xiaobong
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Patturajan, Meera
; APPLICANT: Biallock, Angela
; APPLICANT: Ballinger, Robert
; APPLICANT: Vernet, Corine
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter S
; APPLICANT: Ellerman, Karen
; APPLICANT: Heyes, Melvin P
; APPLICANT: Herrman, John
; APPLICANT: Pena, Carol E A
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Moore, No. US20040010119A11le
; APPLICANT: Shenoy, Suresh
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, Dave
; APPLICANT: Millet, Isabelle
; APPLICANT: Payman, John
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-269
; CURRENT APPLICATION NUMBER: US/10/074,978A
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: 60/268,221
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/335,109
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/312,284
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/268,496
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/276,703
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/330,293
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/322,127
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/280,899
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/310,797
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/268,646
; PRIOR FILING DATE: 2001-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 547

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 18
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-074-978A-18

Query Match 99.3%; Score 1927.5; DB 4; Length 488;
Best Local Similarity 99.5%; Pred. No. 2.7e-142;
Matches 368; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 MYAMKYNKQOCIERDEVRNVFRELEILQIEHVFVNLWYSQDEEDMFVVDLLGGD 60
Db 119 MYAMKYNKQOCIERDEVRNVFRELEILQIEHVFVNLWYSQDEEDMFVVDLLGGD 178
Qy 61 LRYHLOQNVQFSDTVRLYICEMALADYLRGQHIHRDVKPDNILLDERGHAHLTD FNI 120
Db 179 LRYHLOQNVQFSDTVRLYICEMALADYLRGQHIHRDVKPDNILLDERGHAHLTD FNI 238
Qy 121 ATIIKDGERTALAGTKPYMAPEIFHSFVNGGTGYSEVDWWSVGVNAYELLRGWRPYDI 180
Db 239 ATIIKDGERTALAGTKPYMAPEIFHSFVNGGTGYSEVDWWSVGVNAYELLRGWRPYDI 298
Qy 181 HSSNAVESLVQLFSTVSQVYPTWSEKEMWALLRK-LITVNPHEHRLSSLODVQAAPALAGV 239
Db 299 HSSNAVESLVQLFSTVSQVYPTWSEKEMWALLRK-LITVNPHEHRLSSLODVQAAPALAGV 358
Qy 240 LWDHLSEKRVPGFVFNKGRHLCDPTFELEEMILESRLPHKKKRLAKNKS RDNRSRSSQ 299
Db 359 LWDHLSEKRVPGFVFNKGRHLCDPTFELEEMILESRLPHKKKRLAKNKS RDNRSRSSQ 418
Qy 300 SENDYLDCLDAIQDFVIFNREKLKRSQDLPREPLPAPESRDAAPVEDEAERSALPMC 359
Db 419 SENDYLDCLDAIQDFVIFNREKLKRSQDLPREPLPAPESRDAAPVEDEAERSALPMC 478
Qy 360 GPICPSAGSG 369
Db 479 GPICPSAGSG 488

RESULT 10

US-09-819-607-5
; Sequence 5, Application US/09819607
; Publication No. US20030022337A1
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001078
; CURRENT APPLICATION NUMBER: US/09/819,607
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-09-819-607-5

Query Match 96.5%; Score 1873.5; DB 3; Length 368;
Best Local Similarity 97.0%; Pred. No. 3.3e-138;
Matches 358; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

Qy 1 MYAMKYNKQOCIERDEVRNVFRELEILQIEHVFVNLWYSQDEEDMFVVDLLGGD 60
Db 1 MYAMKYNKQOCIERDEVRNVFRELEILQIEHVFVNLWYSQDEEDMFVVDLLGGD 60
Qy 61 LRYHLOQNVQFSDTVRLYICEMALADYLRGQHIHRDVKPDNILLDERGHAHLTD FNI 120
Db 61 LRYHLOQNVQFSDTVRLYICEMALADYLRGQHIHRDVKPDNILLDERGHAHLTD FNI 120
Qy 121 ATIIKDGERTALAGTKPYMAPEIFHSFVNGGTGYSEVDWWSVGVNAYELLRGWRPYDI 180

Db 121 ATIIKDGERTALAGTKPYMAPEIFHSFVNGGTGYSFVDWMSLGMAYELLRGWRPYDI 180
QY 181 HSSNAVESLVQLFSTVSQVYPTWSKEMVALLRKLITVNPHEHRLSSLDQVQAAPALAGVL 240
Db 181 HSSNAVESLVQLFSTVSQVYPTWSREMVALLRKLITVNPHEHRLSSLDQVQAAPALAGVL 240
QY 241 WHLSEKRVPEPFGVPNKGRLHCDPTFELEEMILESRLPKKKRLAKNKSRRNSRDSOS 300
Db 241 WGHLSKRVPEPFGVPNKGRLHCDPTFELEEMILESRLPKKKRLAKNKSRRNSRDSOS 300
QY 301 ENDYLQDCLDAIQDDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
Db 301 ENDYLQDCLDAIQDDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 359
QY 361 PICPSAGSG 369
Db 360 PICPSAGSG 368

RESULT 11
US-10-074-978A-156
; Sequence 156, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
; APPLICANT: Leite, Mario
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Fernandes, Elma
; APPLICANT: Li, Li
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Liu, Xiahong
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Patturajan, Meera
; APPLICANT: Blalock, Angela
; APPLICANT: Ballinger, Robert
; APPLICANT: Vernet, Corine
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter S
; APPLICANT: Ellerman, Karen
; APPLICANT: Herrman, John
; APPLICANT: Pena, Carol E A
; APPLICANT: Shinkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Moore, No. US20040010119A11le
; APPLICANT: Shenoy, Suresh
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, Dave
; APPLICANT: Millet, Isabelle
; APPLICANT: Feyman, John
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-269
; CURRENT APPLICATION NUMBER: US/10/074,978A
; PRIOR FILING DATE: 2003-01-07
; PRIOR FILING DATE: 2001-02-12
; PRIOR FILING DATE: 2001-02-12
; PRIOR FILING DATE: 2001-02-12
; PRIOR FILING DATE: 2001-10-31
; PRIOR FILING DATE: 2001-10-31
; PRIOR FILING DATE: 2001-08-14
; PRIOR FILING DATE: 2001-08-14
; PRIOR FILING DATE: 2001-02-13
; PRIOR FILING DATE: 2001-02-13
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-10-18

; PRIOR APPLICATION NUMBER: 60/322,127
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/280,899
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/310,797
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/268,646
; PRIOR FILING DATE: 2001-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 156
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Macaca fuscata
US-10-074-978A-156
Query Match 96.5%; Score 1873.5; DB 4; Length 368;
Best Local Similarity 97.0%; Pred. No. 3.3e-138;
Matches 358; Conservative 3; Mismatches 7; Indels 1; Gaps 1;
QY 1 MYAMKYNKQOCIERDEVERNVELEILQEIIEHVFVLNLMYSFQDEEDMFVVLLGGD 60
Db 1 MYAMKYNKQOCIERDEVERNVELEILQEIIEHVFVLNLMYSFQDEEDMFVVLLGGD 60
QY 61 LRYHLQONVQPSDETVRLYICEMALADYLROQHIIHRDVKPDNILLDRGHAHLTDFNI 120
Db 61 LRYHLQONVQPSDETVRLYICEMALADYLROQHIIHRDVKPDNILLDRGHAHLTDFNI 120
QY 121 ATIIKDGERTALAGTKPYMAPEIFHSFVNGGTGYSFVDWMSLGMAYELLRGWRPYDI 180
Db 121 ATIIKDGERTALAGTKPYMAPEIFHSFVNGGTGYSFVDWMSLGMAYELLRGWRPYDI 180
QY 181 HSSNAVESLVQLFSTVSQVYPTWSKEMVALLRKLITVNPHEHRLSSLDQVQAAPALAGVL 240
Db 181 HSSNAVESLVQLFSTVSQVYPTWSREMVALLRKLITVNPHEHRLSSLDQVQAAPALAGVL 240
QY 241 WHLSEKRVPEPFGVPNKGRLHCDPTFELEEMILESRLPKKKRLAKNKSRRNSRDSOS 300
Db 241 WGHLSKRVPEPFGVPNKGRLHCDPTFELEEMILESRLPKKKRLAKNKSRRNSRDSOS 300
QY 301 ENDYLQDCLDAIQDDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 360
Db 301 ENDYLQDCLDAIQDDFVIFNREKLKRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCG 359
QY 361 PICPSAGSG 369
Db 360 PICPSAGSG 368
RESULT 12
US-10-633-631-5
; Sequence 5, Application US/10633631
; Publication No. US20040067568A1
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001078DIV
; CURRENT APPLICATION NUMBER: US/10/633,631
; CURRENT FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-10-633-631-5
Query Match 96.5%; Score 1873.5; DB 4; Length 368;
Best Local Similarity 97.0%; Pred. No. 3.3e-138;
Matches 358; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

QY 1 MYAMKMNKQOCIERDEVNRVFRLEILQIEIHVFLVNLWYSFQDEEDMFVVDLLGGD 60
DB 1 MYAMKMNKQOCIERDEVNRVFRLEILQIEIHVFLVNLWYSFQDEEDMFVVDLLGGD 60
QY 61 LRYHLOQNVQFSEDTVRLYICEMALDYLRCQHIIHROVKPDNILLDERGHAHLTDENI 120
DB 61 LRYHLOQNVQFSEDTVRLYICEMALDYLRCQHIIHROVKPDNILLDERGHAHLTDENI 120
QY 121 ATIIKDGERRATAGTKPYMAPEI FHSFVNGGTGYSFVDMWSVGMAYELLRGWRPYDI 180
DB 121 ATIIKDGERRATAGTKPYMAPEI FHSFVNGGTGYSFVDMWSVGMAYELLRGWRPYDI 180
QY 181 HSSNAVESLVQLFSTVSQVYPTWSKEMVALLRKLLTVNPEHRLSSLDQVQAAPALAGVL 240
DB 181 HSSNAVESLVQLFSTVSQVYPTWSKEMVALLRKLLTVNPEHRLSSLDQVQAAPALAGVL 240
QY 241 WDHLSEKRVPGFVPNKGRLHCDPTFELEEMILESRLPKKKKRLAKNKSNDNRSSQS 300
DB 241 WGHLSKRVPGFVPNKGRLHCDPTFELEEMILESRLPKKKKRLAKNKSNDNRSSQS 300
QY 301 ENDYLQDCLDALQDDFVIFNRKLRKSQDLPREPLPAPESRDAAPVEDEAERSALPMCG 360
DB 301 ENDYLQDCLDALQDDFVIFNRKLRKSQDLPREPLPAPESRDAAPVEDE-BSQALPMCG 359
QY 361 PICPSAGSG 369
DB 360 PICPSAGSG 368

RESULT 13
US-10-415-011-12
; Sequence 12, Application US/10415011
; Publication No. US20040053394A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION
; APPLICANT: GURURAJAN, Rajagopal
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: XU, Yuming
; APPLICANT: ARVIZU, Chandra S.
; APPLICANT: YAO, Monique G.
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: DING, Li
; APPLICANT: TANG, Y. Tom
; APPLICANT: HAFALIA, April J.A.
; APPLICANT: NGUYEN, Dannel B.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: LU, Yan
; APPLICANT: YUE, Henry
; APPLICANT: BURFORD, Neil
; APPLICANT: BANDMAN, Olga
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: LAL, Preeti G.
; APPLICANT: RECIPON, Shirley A.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: BOROWSKI, Mark L.
; APPLICANT: THORNTON, Michael B.
; APPLICANT: SWARNAKER, Anita
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: KHAN, Farrah A.
; APPLICANT: ISON, Craig H.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0262 USN
; CURRENT APPLICATION NUMBER: US/10/415,011
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: PCT/US01/47728
; PRIOR FILING DATE: 2001-10-20
; PRIOR APPLICATION NUMBER: US 60/242,410
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/244,068
; PRIOR FILING DATE: 2000-10-27

; PRIOR APPLICATION NUMBER: US 60/245,708
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/247,672
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/249,565
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: US 60/252,730
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/250,807
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PERL Program
; SEQ ID NO 12
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040053394A1 7473788CD1
US-10-415-011-12

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Best Local Similarity 95.4%; Pred. No. 1.8e-134;
Matches 352; Conservative 1; Mismatches 15; Indels 1; Gaps 1;

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QY 61 LRYHLOQNVQFSEDTVRLYICEMALDYLRCQHIIHROVKPDNILLDERGHAHLTDENI 120
DB 178 LRYHLOQNVQFSEDTVRLYICEMALDYLRCQHIIHROVKPDNILLDERGHAHLTDENI 237
QY 121 ATIIKDGERRATAGTKPYMAPEI FHSFVNGGTGYSFVDMWSVGMAYELLRGWRPYDI 180
DB 238 ATIIKDGERRATAGTKPYMAPEI FHSFVNGGTGYSFVDMWSVGMAYELLRGWRPYDI 297
QY 181 HSSNAVESLVQLFSTVSQVYPTWSKEMVALLRKLLTVNPEHRLSSLDQVQAAPALAGVL 240
DB 298 HSSNAVESLVQLFSTVSQVYPTWSKEMVALLRKLLTVNPEHRLSSLDQVQAAPALAGVL 357
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DB 358 WDHLSEKRVPGFVPNKGRLHCDPTFELEEMILESRLPKKKKRLAKNKSNDNRSSQS 417
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DB 418 ENDYLQDCLDALQDDFVIFNRKLRKSQDLPREPLPAPESRDAAPVEDEAERSALPMCG 476
QY 361 PICPSAGSG 369
DB 477 PICPSAGSG 485

RESULT 14
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; Sequence 4, Application US/09819607
; Publication No. US20030022337A1
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01078
; CURRENT APPLICATION NUMBER: US/09/819,607
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-819-607-4

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Query Match          92.0%; Score 1786.5; DB 3; Length 399;
Best Local Similarity 92.4%; Pred. No. 2.3e-131;
Matches 341; Conservative 10; Mismatches 17; Indels 1; Gaps 1;

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Db 31 MYAMKYNKQQCIERDEVNVPFLEILQIEIHVFLVNLWYSFQDEEDFMVVDLLLGSD 90

QY 61 LRYHLQONVQFSEDTVRLVICEMALALDYLRQGHIIHRDVKPDNILLDERGHAHLTD FNI 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 91 LRYHLQONVQFSEDTVRLVICEMALALDYLRQGHIIHRDVKPDNILLDERGHAHLTD FNI 150

QY 121 ATIIKDGERTALAGTKPYMAPEI PHSFVNGGTGYSFEYDWMVSGVMAYELLRGWRPYDI 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 151 ATIIKDGERTALAGTKPYMAPEI PHSFVNGGTGYSFEYDWMVSGVMAYELLRGWRPYDI 210

QY 181 HSSNAVESLVQLFSTVSQVYPTWSEKEMVALLRKLLTVNPEHRLSSLDQVQAAPALAGVL 240
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Db 211 HSSNAVESLVQLFSTVSQVYPTWSEKEMVALLRKLLTVNPEHRLSSLDQVQAAPALAGVL 270

QY 241 WDHLSEKRVPGFVFNKGRHLCDPTFELEEMILESRLHKKKRLAKNKSRRDSSQS 300
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Db 271 WDDLSEKRVPGFVFNKGRHLCDPTFELEEMILESRLHKKKRLAKNKSRRDSSQS 330

QY 301 ENDYLQDCLDALIQDDFVIFNREKLKRSQDLPREPLPAPESRDAARPVED-EAERSALPMC 359
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 331 ENDYLQDCLDALIQDDFVIFNREKLKRSQDLPREPLPAPESRDAARPVED-EAERSALPMC 390

QY 360 GPICPSAGS 368
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Db 391 GSICPSSGS 399

Search completed: May 9, 2006, 10:49:40
Job time : 79 secs
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RESULT 15
US-10-633-631-4
; Sequence 4, Application US/10633631
; Publication No. US20040067568A1
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001078DIV
; CURRENT APPLICATION NUMBER: US/10/633,631
; CURRENT FILING DATE: 2003-08-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-633-631-4
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Query Match          92.0%; Score 1786.5; DB 4; Length 399;
Best Local Similarity 92.4%; Pred. No. 2.3e-131;
Matches 341; Conservative 10; Mismatches 17; Indels 1; Gaps 1;

QY 1 MYAMKYNKQQCIERDEVNVPFLEILQIEIHVFLVNLWYSFQDEEDFMVVDLLLGSD 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 31 MYAMKYNKQQCIERDEVNVPFLEILQIEIHVFLVNLWYSFQDEEDFMVVDLLLGSD 90

QY 61 LRYHLQONVQFSEDTVRLVICEMALALDYLRQGHIIHRDVKPDNILLDERGHAHLTD FNI 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 91 LRYHLQONVQFSEDTVRLVICEMALALDYLRQGHIIHRDVKPDNILLDERGHAHLTD FNI 150

QY 121 ATIIKDGERTALAGTKPYMAPEI PHSFVNGGTGYSFEYDWMVSGVMAYELLRGWRPYDI 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 151 ATIIKDGERTALAGTKPYMAPEI PHSFVNGGTGYSFEYDWMVSGVMAYELLRGWRPYDI 210

QY 181 HSSNAVESLVQLFSTVSQVYPTWSEKEMVALLRKLLTVNPEHRLSSLDQVQAAPALAGVL 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 211 HSSNAVESLVQLFSTVSQVYPTWSEKEMVALLRKLLTVNPEHRLSSLDQVQAAPALAGVL 270
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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 9, 2006, 10:48:24 ; Search time 17 Seconds
(without alignments)
1004.651 Million cell updates/sec

Title: US-10-633-631-2

Perfect score: 1942

Sequence: 1 MYAMKYNKQOCIERDEVRN.....EAERSALPMCGPCPSAGSG 369

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA New:

- 1: /SIDSS5/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 2: /SIDSS5/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /SIDSS5/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /SIDSS5/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 5: /SIDSS5/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 7: /SIDSS5/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 8: /SIDSS5/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 9: /SIDSS5/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 10: /SIDSS5/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 11: /SIDSS5/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 12: /SIDSS5/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1576	81.2	375	9	US-10-979-095-12
2	1249.5	64.3	364	9	US-10-194-487-572
3	1249.5	64.3	364	9	US-10-195-883-572
4	1249.5	64.3	364	9	US-10-195-888-572
5	1249.5	64.3	364	9	US-10-195-889-572
6	1146.5	59.0	396	11	US-11-125-295-11
7	1142	58.8	407	11	US-11-125-295-9
8	709	36.5	225	11	US-11-125-295-5
9	709	36.5	236	11	US-11-125-295-7
10	458	23.6	733	8	US-10-505-928-349
11	444	22.9	740	9	US-10-878-568A-129
12	435.5	22.4	502	11	US-11-188-298-19312
13	435	22.4	385	11	US-11-096-568A-31309
14	435	22.4	424	11	US-11-096-568A-31308
15	435	22.4	471	11	US-11-096-568A-31307
16	433.5	22.3	490	11	US-11-188-298-9166
17	432.5	22.3	480	11	US-11-188-298-1665
18	429.5	22.1	480	11	US-11-132-142-6
19	427.5	22.0	518	11	US-11-188-298-11340
20	426.5	22.0	539	11	US-11-188-298-13310
21	425.5	21.9	522	11	US-11-188-298-1229

ALIGNMENTS

RESULT 1

US-10-979-095-12
; Sequence 12, Application US/10979095
; Publication No. US20060068481A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YANG, Junning
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: BURFORD, Neil
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Dying Aina M.
; APPLICANT: REDDY, Roopa
; APPLICANT: YUE, Henry
; APPLICANT: YAO, Monique G.
; APPLICANT: LAL, Preeti
; APPLICANT: KAHN, Farrah A.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCES: FI-0002 PCT
; CURRENT APPLICATION NUMBER: US/10/979,095
; PRIOR FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/10/168,582
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 60/172,066; 60/176,107; 60/176,107; 60/177,731
; PRIOR FILING DATE: 1999-12-23; 2000-01-14; 2000-01-14; 2000-01-21
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 12
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 3244919CD1
US-10-979-095-12

Query Match 81.2%; Score 1576; DB 9; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.1e-114;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MYAMKYNKQOCIERDEVRNVELETLQIEHVFVLNLYSFQDEEDMFVVDLLGGD 60
Db 51 MYAMKYNKQOCIERDEVRNVELETLQIEHVFVLNLYSFQDEEDMFVVDLLGGD 110
Qy 61 LRVHLQNVQFSBTVRLYICEMALDYLKGGQIHRDVKPNILLDERGHAHLDFNI 120

Db 111 LRVHLQNVQFSEDVRLVYICEMALDYLRGQHIHRRDKPDNILLDERGHAHLTDFNI 170
QY 121 ATKIGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGMAYELLRGWRPYDI 180
Db 171 ATKIGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGMAYELLRGWRPYDI 230
QY 181 HSSNAVESLVOLFSTVSQVPTWSKEMVALLRKLTVNPEHRLSSLDVQAAPALAGVL 240
Db 231 HSSNAVESLVOLFSTVSQVPTWSKEMVALLRKLTVNPEHRLSSLDVQAAPALAGVL 290
QY 241 WDLSEKRVPGFVFNKGRHLCDPTFELEEMILESRLHKKKRLAKNKSNDSSOS 300
Db 291 WDLSEKRVPGFVFNKGRHLCDPTFELEEMILESRLHKKKRLAKNKSNDSSOS 350
RESULT 2
US-10-194-487-572
; Sequence 572, Application US/10194487
; Publication No. US20060074226A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C312
; CURRENT APPLICATION NUMBER: US/10/194,487
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 572
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-194-487-572
Query Match 64.3%; Score 1249.5; DB 9; Length 364;
Best Local Similarity 69.2%; Pred. No. 2.2e-89;
Matches 225; Conservative 50; Mismatches 49; Indels 1; Gaps 1;
QY 4 MKYMNKQCIERDEVNRFRELEIQEIEHVFVNLWYSFQDEDMFMVVDLLGGDLRY 63
Db 1 MKYMNKQCIERDEVNRFRELEIQEIEHVFVNLWYSFQDEDMFMVVDLLGGDLRY 60

QY 64 HLQQNVQFSEDVRLVYICEMALDYLRGQHIHRRDKPDNILLDERGHAHLTDFNIAT 123
Db 61 HLQQNVHFTGTVKLYICELALALEYLQRYHIHRDIKPDNILLDEGHVHITDFNIATV 120
QY 124 IKDGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGMAYELLRGWRPYDIHSS 183
Db 121 VKGAERASSMAGTKPYMAPEVQVYMDRPGYSGYPVDMWSLGITAYELLRGWRPYEHSV 180
QY 184 NAVESLVOLFSTVSQVPTWSKEMVALLRKLTVNPEHRLSSLDVQAAPALAGVLWDH 243
Db 181 TPIDEILNMFKRVYHYSSTWCKGMVALLRKLTKDPESRVSLHDIQSVPYLADNMWDA 240
QY 244 LSEKRVPGFVFNKGRHLCDPTFELEEMILESRLHKKKRLAKNKSNDSSOS 303
Db 241 VFKKALMPGFVFNKGRHLCDPTFELEEMILESRLHKKKRLAKNKSNDSSOS 303
QY 304 YLQDCLDAIQODFVFNREKLRSQ 328
Db 300 HLQHCLETVREBFIFNREKLRRQ 324
RESULT 3
US-10-195-883-572
; Sequence 572, Application US/10195883
; Publication No. US20060073544A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C323
; CURRENT APPLICATION NUMBER: US/10/195,883
; CURRENT FILING DATE: 2002-07-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 572
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-195-883-572
Query Match 64.3%; Score 1249.5; DB 9; Length 364;
Best Local Similarity 69.2%; Pred. No. 2.2e-89;
Matches 225; Conservative 50; Mismatches 49; Indels 1; Gaps 1;
QY 4 MKYMNKQCIERDEVNRFRELEIQEIEHVFVNLWYSFQDEDMFMVVDLLGGDLRY 63
Db 1 MKYMNKQCIERDEVNRFRELEIQEIEHVFVNLWYSFQDEDMFMVVDLLGGDLRY 60
QY 64 HLQQNVQFSEDVRLVYICEMALDYLRGQHIHRRDKPDNILLDERGHAHLTDFNIAT 123
Db 61 HLQQNVHFTGTVKLYICELALALEYLQRYHIHRDIKPDNILLDEGHVHITDFNIATV 120
QY 124 IKDGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGMAYELLRGWRPYDIHSS 183
Db 121 VKGAERASSMAGTKPYMAPEVQVYMDRPGYSGYPVDMWSLGITAYELLRGWRPYEHSV 180
QY 184 NAVESLVOLFSTVSQVPTWSKEMVALLRKLTVNPEHRLSSLDVQAAPALAGVLWDH 243
Db 181 TPIDEILNMFKRVYHYSSTWCKGMVALLRKLTKDPESRVSLHDIQSVPYLADNMWDA 240
QY 244 LSEKRVPGFVFNKGRHLCDPTFELEEMILESRLHKKKRLAKNKSNDSSOS 303
Db 241 VFKKALMPGFVFNKGRHLCDPTFELEEMILESRLHKKKRLAKNKSNDSSOS 303

Qy 304 YLQDCLDAIQODFVIFNREKLRKRSQ 328
 Db 300 HLQHCLETVREEFIIFNREKLRKRSQ 324

RESULT 4

US-10-195-888-572
 ; Sequence 572, Application US/10195888
 ; Publication No. US20060073545A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P343OR1C324
 ; CURRENT FILING DATE: 2002-07-15
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 572
 ; LENGTH: 364
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-195-888-572

Query Match 64.3%; Score 1249.5; DB 9; Length 364;
 Best Local Similarity 69.2%; Pred. No. 2.2e-89;
 Matches 225; Conservative 50; Mismatches 49; Indels 1; Gaps 1;

Qy 4 MKNMKNQOCIERDEVRNVFRELQIEIHVFLVNLWYSFQDEEDMFVVDLLGGDLRY 63
 Db 1 MKNMKNQOCIERDEVRNVFRELQIEIHVFLVNLWYSFQDEEDMFVVDLLGGDLRY 60
 Qy 64 HLOQNVQFSEDTYRLYICEMALDYLRGQHIHRDVKPNILDERGHAHLTDNFNATI 123
 Db 61 HLOQNVHFTGTVKLYICELALALEYLQRYHIHRDIKPNILDERGHAHLTDNFNATI 120
 Qy 124 IKDGERATAGTKPYMAPEIFHSFVNGGTGYSFVDWWSVGMAYELLRGWRPYDIHSS 183
 Db 121 VKGAERASSMAGTKPYMAPEVQVYMDRGPYSDVWWSLIGITAYELLRGWRPYEIHVS 180
 Qy 184 NAVESLVQLFSTVSQVPTWKSKEVALLKLLTVNPEHLRSLSSLDVQVQAPALAGVLDWH 243
 Db 181 TPDIILNMFKVERVHYSSVTKGKVALLLKLLTKDPESRVSSLDIQQSVPYLADNMWDA 240
 Qy 244 LSEKRVPGVPNGKRLHCDPTFELEEMILESPLHKKKRLAKNKRSDNSRDSQSSEND 303
 Db 241 VFKKALMPGVPNGKRLNCDPTFELEEMILESPLHKKKRLAKNKRSDGTDKDCPL-NG 299
 Qy 304 YLQDCLDAIQODFVIFNREKLRKRSQ 328
 Db 300 HLQHCLETVREEFIIFNREKLRKRSQ 324

RESULT 5

US-10-195-889-572
 ; Sequence 572, Application US/10195889
 ; Publication No. US20060074227A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P343OR1C329
 ; CURRENT FILING DATE: 2002-07-15
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 572
 ; LENGTH: 364
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-195-889-572

Query Match 64.3%; Score 1249.5; DB 9; Length 364;
 Best Local Similarity 69.2%; Pred. No. 2.2e-89;
 Matches 225; Conservative 50; Mismatches 49; Indels 1; Gaps 1;

Qy 4 MKNMKNQOCIERDEVRNVFRELQIEIHVFLVNLWYSFQDEEDMFVVDLLGGDLRY 63
 Db 1 MKNMKNQOCIERDEVRNVFRELQIEIHVFLVNLWYSFQDEEDMFVVDLLGGDLRY 60
 Qy 64 HLOQNVQFSEDTYRLYICEMALDYLRGQHIHRDVKPNILDERGHAHLTDNFNATI 123
 Db 61 HLOQNVHFTGTVKLYICELALALEYLQRYHIHRDIKPNILDERGHAHLTDNFNATI 120
 Qy 124 IKDGERATAGTKPYMAPEIFHSFVNGGTGYSFVDWWSVGMAYELLRGWRPYDIHSS 183
 Db 121 VKGAERASSMAGTKPYMAPEVQVYMDRGPYSDVWWSLIGITAYELLRGWRPYEIHVS 180
 Qy 184 NAVESLVQLFSTVSQVPTWKSKEVALLKLLTVNPEHLRSLSSLDVQVQAPALAGVLDWH 243
 Db 181 TPDIILNMFKVERVHYSSVTKGKVALLLKLLTKDPESRVSSLDIQQSVPYLADNMWDA 240
 Qy 244 LSEKRVPGVPNGKRLHCDPTFELEEMILESPLHKKKRLAKNKRSDNSRDSQSSEND 303
 Db 241 VFKKALMPGVPNGKRLNCDPTFELEEMILESPLHKKKRLAKNKRSDGTDKDCPL-NG 299
 Qy 304 YLQDCLDAIQODFVIFNREKLRKRSQ 328
 Db 300 HLQHCLETVREEFIIFNREKLRKRSQ 324

RESULT 6
 US-11-125-295-11
 ; Sequence 11, Application US/11125295
 ; Publication No. US20050287562A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hu, Yi
 ; APPLICANT: Nepomnichy, Boris
 ; APPLICANT: Wang, Xiaoming
 ; APPLICANT: Donoho, Gregory
 ; APPLICANT: Scoville, John
 ; APPLICANT: Walke, D. Wade
 ; TITLE OF INVENTION: Novel Human Kinase Proteins and Polynucleotides Encoding the Same
 ; FILE REFERENCE: LEX-0167-USA
 ; CURRENT FILING DATE: 2005-05-09
 ; Prior Application Number: US/11/125,295
 ; Prior Filing Date: 2003-07-15
 ; Prior Application Number: US/09/841,683
 ; Prior Filing Date: 2001-04-24
 ; Prior Application Number: US 60/199,499
 ; Prior Filing Date: 2000-04-25
 ; Prior Application Number: US 60/201,227
 ; Prior Filing Date: 2000-05-01
 ; NUMBER OF SEQ ID NOS: 12

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 396
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-125-295-11

Query Match      59.0%; Score 1146.5; DB 11; Length 396;
Best Local Similarity 63.1%; Pred. No. 2.3e-81;
Matches 219; Conservative 47; Mismatches 72; Indels 9; Gaps 3;

QY 1 MYAMKYNKQOCIERDEVNVPFELQIEIHVFLVNLWYSFQDEEDMFVVDDLGLGD 60
DB 48 MYAMKYNKQOCVERNEVNFVKELQIMQGLEHFLVNLWYSFQDEEDMFVVDDLGLGD 107
QY 61 LRYHLQONVQFSEDVRLYVICEMALALDYLRGQHHIHRDVKPDNILLDERGHAHLTDFNI 120
DB 108 LRYHLQONVHFKEETVKLFICELVWALDYLRGQHHIHRDMKPDNILLDEHGHVHITDFNI 167
QY 121 ATIIKDGERRATAGTKPYMAPBIFHSFVNGGTGYSFVDMWSVGMAYELLRGWRPYDI 180
DB 168 AAMLPRETOITTMAGTKPYMAPEMPSS--RKAGAGYSFAVDMWSLGVATAYELLRGRRPYHI 225
QY 181 HSNVAVESLVOLFSTVSVOYVPTWSEKEMVALLKRLITVNPHEHRLSSLODVQAAPALAGVL 240
DB 226 RSTSKSEIVHTFETTVTPYPSAWSQEMVSLKKLEPNPDQRFQSLSDVQNFPPYNDIN 285
QY 241 WHLSEKRVPEPGFVPNKGRLHCDPTFELBEMILESPLHKKKRLAKNKSRRNSRDSQS 300
DB 286 WDAVFQKRLIPGPIPNKGRINCPTFELBEMILESPLHKKKRLAKKEMKRCDSST 345
QY 301 ENDYLODCLDATQDDVFVFNREKL-----KRSQDLPREPLPAPESRD 342
DB 346 --CLLQEHLDVQKEPIIFNREKVRNDFNKRQPNLALEQTKDPQGED 390

RESULT 7
US-11-125-295-9
; Sequence 9, Application US/11125295
; Publication No. US20050287562A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: Novel Human Kinase Proteins and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/11/125,295
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US/10/620,845
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/841,683
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 407
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-125-295-9

Query Match      58.8%; Score 1142; DB 11; Length 407;
Best Local Similarity 63.2%; Pred. No. 5.4e-81;
Matches 216; Conservative 50; Mismatches 72; Indels 4; Gaps 2;

QY 1 MYAMKYNKQOCIERDEVNVPFELQIEIHVFLVNLWYSFQDEEDMFVVDDLGLGD 60
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DB 48 MYAMKYNKQOCVERNEVNFVKELQIMQGLEHFLVNLWYSFQDEEDMFVVDDLGLGD 107
QY 61 LRYHLQONVQFSEDVRLYVICEMALALDYLRGQHHIHRDVKPDNILLDERGHAHLTDFNI 120
DB 108 LRYHLQONVHFKEETVKLFICELVWALDYLRGQHHIHRDMKPDNILLDEHGHVHITDFNI 167
QY 121 ATIIKDGERRATAGTKPYMAPBIFHSFVNGGTGYSFVDMWSVGMAYELLRGWRPYDI 180
DB 168 AAMLPRETOITTMAGTKPYMAPEMPSS--RKAGAGYSFAVDMWSLGVATAYELLRGRRPYHI 225
QY 181 HSNVAVESLVOLFSTVSVOYVPTWSEKEMVALLKRLITVNPHEHRLSSLODVQAAPALAGVL 240
DB 226 RSTSKSEIVHTFETTVTPYPSAWSQEMVSLKKLEPNPDQRFQSLSDVQNFPPYNDIN 285
QY 241 WHLSEKRVPEPGFVPNKGRLHCDPTFELBEMILESPLHKKKRLAKNKSRRNSRDSQS 300
DB 286 WDAVFQKRLIPGPIPNKGRINCPTFELBEMILESPLHKKKRLAKKEMKRCDSST 345
QY 301 ENDYLODCLDATQDDVFVFNREKLKRSQDLPREPLPAPESRD 342
DB 346 --CLLQEHLDVQKEPIIFNREKVRNDFNKRQPNLALEQTKD 385

RESULT 8
US-11-125-295-5
; Sequence 5, Application US/11125295
; Publication No. US20050287562A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: Novel Human Kinase Proteins and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/11/125,295
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US/10/620,845
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: US/09/841,683
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 60/199,499
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/201,227
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 225
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-125-295-5

Query Match      36.5%; Score 709; DB 11; Length 225;
Best Local Similarity 74.1%; Pred. No. 8.8e-48;
Matches 129; Conservative 21; Mismatches 22; Indels 2; Gaps 1;

QY 1 MYAMKYNKQOCIERDEVNVPFELQIEIHVFLVNLWYSFQDEEDMFVVDDLGLGD 60
DB 48 MYAMKYNKQOCVERNEVNFVKELQIMQGLEHFLVNLWYSFQDEEDMFVVDDLGLGD 107
QY 61 LRYHLQONVQFSEDVRLYVICEMALALDYLRGQHHIHRDVKPDNILLDERGHAHLTDFNI 120
DB 108 LRYHLQONVHFKEETVKLFICELVWALDYLRGQHHIHRDMKPDNILLDEHGHVHITDFNI 167
QY 121 ATIIKDGERRATAGTKPYMAPBIFHSFVNGGTGYSFVDMWSVGMAYELLRG 174
DB 168 AAMLPRETOITTMAGTKPYMAPEMPSS--RKAGAGYSFAVDMWSLGVATAYELLRG 219

RESULT 9
US-11-125-295-7
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```

; Sequence 7, Application US/11125295
; Publication No. US20050287562A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Yi
; APPLICANT: Nepomniichy, Boris
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Walke, D. Wade
; TITLE OF INVENTION: Novel Human Kinase Proteins and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0167-USA
; CURRENT APPLICATION NUMBER: US/11/125,295
; PRIOR FILING DATE: 2005-05-09
; PRIOR FILING DATE: 2003-07-15
; PRIOR FILING DATE: 2000-04-25
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 236
; TYPE: PRT
; ORGANISM: homo sapiens
; US-11-125-295-7

Query Match      36.5%; Score 709; DB 11; Length 236;
Best Local Similarity 74.1%; Pred. No. 9.3e-48;
Matches 129; Conservative 21; Mismatches 22; Indels 2; Gaps 1;

QY 1 MYAMKYNKQOCIERDEVRNVFRELEILOEIHVFLVNLWYSFQDEEDMFVVDLLGGD 60
DB 48 MYAMKYNKQOCVERNEVRNVFKELQIMQGLEHFPFLVNLWYSFQDEEDMFVVDLLGGD 107
QY 61 LRYHLOONVQFSDTVRLYICEMALDYLRGQHIHRDVKPNILLDERGHAHLTD FNI 120
DB 108 LRYHLOONVHFKEVKELFCFELVMDLYLQNRQIHRDMKPNILLDEGHVHITD FNI 167
QY 121 ATIKDGERATAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVYAYELLRG 174
DB 168 AAMLPRETQITTWAGTKPYMAPEMFSS--RKGAGYSFAVDWWSLGVTA YELLRG 219

RESULT 10
US-10-505-928-349
; Sequence 349, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 349
; LENGTH: 733
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-505-928-349

Query Match      23.6%; Score 458; DB 8; Length 733;
Best Local Similarity 37.5%; Pred. No. 1.1e-27;
Matches 103; Conservative 51; Mismatches 103; Indels 18; Gaps 6;

QY 1 MYAMKYNKQOCIERDEVRNVFRELEILOEIHVFLVNLWYSFQDEEDMFVVDLLGGD 60
DB 87 LYAMKVLKATLKYRDRVRSKM-ERDILAEVNHFFIVKLHYAFQTECKLYILDFLGGD 145
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QY 61 LRYHLOONVQFSDTVRLYICEMALDYLRGQHIHRDVKPNILLDERGHAHLTD FNI 120
DB 146 LFTRLSKEVMFTBEDVKFVLAELALDLHLSGLIYRDLKPNILLDESGHIKITD FGL 205
QY 121 A-TIIKDGERTALAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVYAYELLRGWTPYD 179
DB 206 SKEAIDHKRAVSFCGTVEYMAPEVNNR-----RGHTQSADWWSFGVLMFEMLTGSLP FQ 260
QY 180 IHSSNAVESLQVLFSTVSQYVPTWSEKEMVALLRKLTLVNPHEHRLSS----LQDVQAAPA 235
DB 261 GKDKKETMALILKAKLGMPOFL---SSEAQSLRLMLFKRNPANRLGAGIDGVEIKRHPF 317
QY 236 LAGVLDHLSERKVEFGFVFNKGR-----LHCDPTF 266
DB 318 FVTIDNNTLYRKEIKPPFKPAVGRPEDTFFYDFPEF 352

RESULT 11
US-10-878-556A-129
; Sequence 129, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
; LENGTH: 740
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: sw_hum/k6a3_human
; DATABASE ENTRY DATE: 1996-10-01
; US-10-878-556A-129

Query Match      22.9%; Score 444; DB 9; Length 740;
Best Local Similarity 36.4%; Pred. No. 1.4e-26;
Matches 100; Conservative 52; Mismatches 105; Indels 18; Gaps 6;

QY 1 MYAMKYNKQOCIERDEVRNVFRELEILOEIHVFLVNLWYSFQDEEDMFVVDLLGGD 60
DB 96 LYAMKVLKATLKYRDRVRTKM-ERDILVEVNHFPFIVKLHYAFQTECKLYILDFLGGD 154
QY 61 LRYHLOONVQFSDTVRLYICEMALDYLRGQHIHRDVKPNILLDERGHAHLTD FNI 120
DB 155 LFTRLSKEVMFTBEDVKFVLAELALDLHLSGLIYRDLKPNILLDESGHIKITD FGL 214
QY 121 ATIKDGE-RATLAGTKPYMAPEIFHSFVNGGTGYSFEVDWWSVGVYAYELLRGWTPYD 179
DB 215 SKESIDHEKKAYSFCGTVEYMAPEVNNR-----RGHTQSADWWSFGVLMFEMLTGTL PFO 269
QY 180 IHSSNAVESLQVLFSTVSQYVPTWSEKEMVALLRKLTLVNPHEHRLSS----LQDVQAAPA 235
DB 270 GKDKKETMALILKAKLGMPOFL---SSEAQSLRLMLFKRNPANRLGAGIDGVEIKRHPF 326
QY 236 LAGVLDHLSERKVEFGFVFNKGR-----LHCDPTF 266
DB 327 FSTIDNNTLYRKEIHPFKPATGRPEDTFFYDFPEF 361

RESULT 12
US-11-188-298-19312
; Sequence 19312, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
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